

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:41:36 ; Search time 39 Seconds
(without alignment)
186.075 Million cell updates/sec

Title: US-10-612-885A-1
Perfect score: 117
Sequence: 1 QRVLEIGRTECVLSNLRGTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	109	93.2	316	11 O35545	O35545 rattus norv
2	107	91.5	509	6 Q9MYZ9	Q9MYZ9 sus scrofa
3	104	88.9	229	6 Q28206	Q28206 bos taurus
4	104	88.9	229	6 Q27950	Q27950 bos indicus
5	104	88.9	387	6 Q95N13	Q95N13 ovis aries
6	104	88.9	418	6 Q95N14	Q95N14 ovis aries
7	56	47.9	176	17 Q8TYF5	Q8TYF5 methanopyru
8	52	44.4	1028	4 Q9UQ52	Q9UQ52 homo sapien
9	49	41.9	826	2 Q9AXX8	Q9AXX8 legionella
10	49	41.9	1028	11 P97528	P97528 rattus norv
11	48	41.0	428	10 Q9LPY7	Q9LPY7 arabidopsis
12	48	41.0	1028	11 Q9JMB8	Q9JMB8 mus musculu
13	48	41.0	1028	11 Q8G6X1	Q8G6X1 mus musculu
14	47	40.2	539	10 Q94LS6	Q94LS6 oryza sativ
15	47	40.2	539	10 Q7XDN4	Q7XDN4 oryza sativ
16	47	40.2	640	10 Q9ASX3	Q9ASX3 arabidopsis

17	47	40.2	644	10 Q8LDV1	Q8LDV1 arabidopsis
18	47	40.2	644	10 Q9FNK3	Q9FNK3 arabidopsis
19	47	40.2	1226	16 Q7UL12	Q7UL12 rhodospirell
20	47	40.2	1873	10 Q9FGI1	Q9FGI1 rhodospirell
21	46	39.3	288	12 Q98214	Q98214 molluscum c
22	46	39.3	637	5 Q86GJ9	Q86GJ9 dictyosteli
23	46	39.3	700	11 Q9CXF5	Q9CXF5 mus musculu
24	46	39.3	700	11 Q8C0B3	Q8C0B3 mus musculu
25	46	39.3	781	15 Q82857	Q82857 lembrana di
26	46	39.3	1283	5 Q8TA82	Q8TA82 caenorhabdi
27	45.5	38.9	95	3 Q8TF83	Q8TF83 agroclybe ae
28	45	38.5	76	7 Q30734	Q30734 macaca neme
29	45	38.5	76	7 Q30567	Q30567 macaca fasc
30	45	38.5	81	7 Q30747	Q30747 macaca neme
31	45	38.5	316	16 Q912J3	Q912J3 pseudomonas
32	45	38.5	446	10 Q94CT7	Q94CT7 oryza sativ
33	45	38.5	479	5 Q9U7P5	Q9U7P5 eufolliculi
34	45	38.5	567	5 Q95R48	Q95R48 drosophila
35	45	38.5	567	5 Q9VCA3	Q9VCA3 drosophila
36	45	38.5	773	16 Q8A0C0	Q8A0C0 bacteroides
37	45	38.5	968	5 Q7Y247	Q7Y247 cryptospori
38	45	38.5	1056	12 Q57161	Q57161 spinach lat
39	44.5	38.0	691	5 Q9VML1	Q9VML1 drosophila
40	44.5	38.0	693	5 Q96680	Q96680 drosophila
41	44.5	38.0	810	10 Q92W13	Q92W13 cucurbita m
42	44	37.6	47	16 Q8XFL2	Q8XFL2 salmonella
43	44	37.6	195	16 Q820G3	Q820G3 anabaena sp
44	44	37.6	606	5 Q9VWF6	Q9VWF6 drosophila
45	44	37.6	2023	12 Q91632	Q91632 cherry gree

ALIGNMENTS

RESULT 1

O35545 PRELIMINARY; PRT; 316 AA.
ID AC O35545
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OS Intron 5-inserted form of erythropoietin receptor precursor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98296111; PubMed=9630610;
RA Yamaji R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,
RA Miyatake K., Nakano Y.,
RT "The intron 5-inserted form of rat erythropoietin receptor is
expressed as a membrane-bound form."
RL Biochim. Biophys. Acta 1403:169-178(1998).
DR EMBL; D83509; BAA22373.1; -
DR HSSP; P19235; 1EBA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004892; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004892; F:receptor activity; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemopoetn_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 316 POTENTIAL.
SQ SEQUENCE 316 AA; 34220 MW; 05C44BF8516C180B CRC64;

Query Match 93.2%; Score 109; DB 11; Length 316;
Best Local Similarity 91.3%; Pred. No. 6.8e-10;

Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVVEILGRTECVLSNLRGTRY 23
DB 193 QVVEILGRTECVLSNLRGTRY 215

RESULT 2
Q9MY29 PRELIMINARY; PRT; 509 AA.

AC Q9MY29 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Erythropoietin receptor.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Pearson P.L.; Smith T.P.L.; Sonstegard T.S.; Klemcke H.G.;
RA Christensen R.K.; Vallier J.L.;
RT "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in
RT Embryonic and Fetal Liver."
RL Domest. Anim. Endocrinol. 0:0-0(2000).
DR EMBL; AF274305; AAF77065.1; -.
DR HSSP; P19235; IEBA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003528; Hematopoptn_L_Fl.
DR InterPro; IPR000572; Oxidored_molylb.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Receptor.
SQ SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCD8A CRC64;

Query Match 91.5%; Score 107; DB 6; Length 509;
Best Local Similarity 91.3%; Pred. No. 2.5e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVVEILGRTECVLSNLRGTRY 23
DB 195 QVVEILGRTECVLSNLRGTRY 217

RESULT 3
Q28206 PRELIMINARY; PRT; 229 AA.

AC Q28206 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE Erythropoietin receptor (fragment).
GN EPOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

Query Match 91.3%; Score 107; DB 6; Length 509;
Best Local Similarity 91.3%; Pred. No. 2.5e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVVEILGRTECVLSNLRGTRY 23
DB 195 QVVEILGRTECVLSNLRGTRY 217

RESULT 3
Q28206 PRELIMINARY; PRT; 229 AA.

AC Q28206 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE Erythropoietin receptor (fragment).
GN EPOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

Query Match 91.3%; Score 107; DB 6; Length 509;
Best Local Similarity 91.3%; Pred. No. 2.5e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVVEILGRTECVLSNLRGTRY 23
DB 195 QVVEILGRTECVLSNLRGTRY 217

DR EMBL; U61399; AAB03871.1; -.
DR HSSP; P19235; IEBA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003528; Hematopoptn_L_Fl.
DR InterPro; IPR000572; Oxidored_molylb.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
FT NON_TER 229 229
SQ SEQUENCE 229 AA; 25170 MW; EDFAA6F110D992E8 CRC64;

Query Match 88.9%; Score 104; DB 6; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVVEILGRTECVLSNLRGTRY 23
DB 136 QVVEILGRTECVLSNLRGTRY 158

RESULT 4
Q27950 PRELIMINARY; PRT; 229 AA.

AC Q27950 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE Erythropoietin receptor (fragment).
GN EPOR.
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

Query Match 88.9%; Score 104; DB 6; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVVEILGRTECVLSNLRGTRY 23
DB 136 QVVEILGRTECVLSNLRGTRY 158

RESULT 4
Q27950 PRELIMINARY; PRT; 229 AA.

AC Q27950 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE Erythropoietin receptor (fragment).
GN EPOR.
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

Query Match 88.9%; Score 104; DB 6; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVVEILGRTECVLSNLRGTRY 23
DB 136 QVVEILGRTECVLSNLRGTRY 158

RESULT 5
Q95N13 PRELIMINARY; PRT; 229 AA.

AC Q95N13 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE Erythropoietin receptor (fragment).
GN EPOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Suliman H.B.; Feldman B.F.; Majiwa P.A.O.; Logan-Henfrey L.L.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

Query Match 88.9%; Score 104; DB 6; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Q95N13 PRELIMINARY; PRT; 387 AA.
AC Q95N13;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in
RT the ovine fetus."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY029232; AAK38737.1; -
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004896; F-hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN-III-like.
DR InterPro; IPR003528; Hemopoptn_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR NON_TER.
FT NON_TER
FT NON_TER
SQ SEQUENCE 387 AA; 42039 MW; 0D1E6173432EBC6 CRC64;
Query Match 88.9%; Score 104; DB 6; Length 387;
Best Local Similarity 87.0%; Pred. No. 5.9e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 QRVLEIGRTECVLSNLRGTRY 23
Db 130 QRVLEIGRTECVLSNLRGTRY 152
RESULT 6
Q95N14 PRELIMINARY; PRT; 418 AA.
AC Q95N14;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in
RT the ovine fetus."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY029231; AAK38170.1; -
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004896; F-hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR NON_TER.
FT NON_TER
FT NON_TER
SQ SEQUENCE 418 AA; 45282 MW; BB742EBEA034503C CRC64;
Query Match 88.9%; Score 104; DB 6; Length 418;
Best Local Similarity 87.0%; Pred. No. 6.4e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 QRVLEIGRTECVLSNLRGTRY 23
Db 130 QRVLEIGRTECVLSNLRGTRY 152
RESULT 7
Q8TYF5 PRELIMINARY; PRT; 176 AA.
AC Q8TYF5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Uncharacterized protein.
GN MK0345.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Scherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozvavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
DR ENBL; AS010332; AAM01560.1; -
DR InterPro; IPR009003; Cys_Ser_trypsin.
KW Complete proteome.
SQ SEQUENCE 176 AA; 19285 MW; 81E181C7BF3BBD8B CRC64;
Query Match 47.9%; Score 56; DB 17; Length 176;
Best Local Similarity 52.4%; Pred. No. 0.3;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 2 RVEILGRTECVLSNLRGTR 22
Db 150 RMDVIERTERALKRLRGQR 170
RESULT 8
Q9UQ52 PRELIMINARY; PRT; 1028 AA.
AC Q9UQ52;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neural adhesion molecule NB-3.
GN HNB-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98146168; PubMed=9486763;
RX Kamei Y., Teutsuni O., Taketani Y., Watanabe K.;
RT "cDNA cloning and chromosomal localization of neural adhesion
RT molecule, NB-3 in human.";
RL J. Neurosci. Res. 51:275-283 (1998).
DR ENBL; AB003592; BAA82612.1; -
DR HSSP; P20241; 1CFB.
DR Genew; HGNC:2176; CNTN6.
DR GO; GO:0007155; P:cell adhesion; TAS.

OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.

RESULT 12

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Q9JMB8
ID Q9JMB8 PRELIMINARY; PRT; 1028 AA.
AC Q9JMB8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neural recognition molecule NB-3.
GN CNTN6 OR MNB-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=129SVJ; TISSUE=Brain;
RX MEDLINE=20183687; PubMed=10717476;
RA Lee S., Takeda Y., Kawano H., Haseya H., Nomoto M., Fujimoto D.,
RA Takahashi N., Watanabe K.;
RT "Expression and regulation of a gene encoding neural recognition
RT molecule NB-3 of the contactin/F3 subgroup in mouse brain.";
RL Gene 245:253-266(2000).
CC -1- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
DR ENBL; AB032602; BA92367.1; -.
DR HSP; P20241; ICFB.
DR MGD; MGI:1858223; Cntn6.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; Ig; 6.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.
DR PROSITE; PS00835; IG_LIKE; 6.
DR PROSITE; PS00230; IG_MHC; 1.
SQ IMMUNOGLOBULIN domain.
KW SEQUENCE 1028 AA; 113759 MW; ABEC59F86CA3978F CRC64;

Query Match 41.0%; Score 48; DB 11; Length 1028;
Best Local Similarity 64.3%; Pred.No. 47;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 EGRTECVLSNLRG 20
Db 292 EGFYECIAGNLRG 305

RESULT 13
Q8C6X1 PRELIMINARY; PRT; 1028 AA.
AC Q8C6X1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Contactin 6.
GN CNTN6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
```

```
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK052972; BAC35227.1; -.
DR MGD; MGI:1858223; Cntn6.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; Ig; 6.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 6.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.
DR PROSITE; PS00835; IG_LIKE; 6.
DR PROSITE; PS00230; IG_MHC; 1.
SQ SEQUENCE 1028 AA; 113761 MW; B233BD300881B101 CRC64;

Query Match 41.0%; Score 48; DB 11; Length 1028;
Best Local Similarity 64.3%; Pred.No. 47;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 EGRTECVLSNLRG 20
Db 292 EGFYECIAGNLRG 305

RESULT 14
Q94LS6 PRELIMINARY; PRT; 539 AA.
ID Q94LS6;
AC Q94LS6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Teifrin T.,
RA Riggs F., Heiao J., Zismann V., Blunt S., Pai G., VanAken S.S.,
RA Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNB0011A08 genomic sequence.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AC034258; AAKS4287.1; -.
DR Gramene; Q94LS6; -.
KW Hypothetical protein.
SQ SEQUENCE 539 AA; 60201 MW; 8EBED40239310BC2 CRC64;

Query Match 40.2%; Score 47; DB 10; Length 539;
Best Local Similarity 56.2%; Pred.No. 34;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 EILEGRTECVLSNLRG 19
Db 9 EVHGTSCVLLNVRG 24

RESULT 15
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:40:41 ; Search time 11 seconds
(without alignments)
108.874 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVLEIGRTECVLSNLRGTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	117	100.0	508	1	EPOR_HUMAN
2	109	93.2	507	1	EPOR_MOUSE
3	109	93.2	507	1	EPOR_RAT
4	49	41.9	221	1	GIDB_BIFLO
5	49	41.9	473	1	KRM1_MOUSE
6	49	41.9	475	1	KRM1_HUMAN
7	48	41.0	312	1	PYRB_COREP
8	48	41.0	312	1	PYRB_CORGL
9	47	40.2	956	1	TSF3_HUMAN
10	46	39.3	58	1	YS59_ENTFA
11	46	39.3	67	1	RS28_KLULA
12	46	39.3	67	1	RS28_KLUMA
13	46	39.3	489	1	C128_MCTU
14	46	39.3	697	1	AMS2_SCHPO
15	46	39.3	1609	1	YL54_CABEL
16	45.5	38.9	607	1	DB10_NICSY
17	45	38.5	512	1	YR33_MYCTU
18	45	38.5	1036	1	AX01_CHICK
19	44	37.6	473	1	KRM1_RAT
20	43.5	37.2	269	1	FPG_VIBPA
21	43	36.8	486	1	MURC_CORGL
22	43	36.8	956	1	TSF3_MOUSE
23	42.5	36.3	228	1	YAZ9_TREPA
24	42.5	36.3	1912	1	PTFD_HUMAN
25	42	35.9	67	1	RS28_YEAST
26	42	35.9	365	1	DHAS_YEAST
27	42	35.9	482	1	THII_SALTI
28	42	35.9	482	1	THII_SALTY
29	42	35.9	661	1	HCYC_PANIN
30	42	35.9	1020	1	CONT_MOUSE
31	42	35.9	1021	1	CONT_RAT
32	41.5	35.5	1897	1	PTPF_HUMAN
33	41	35.0	94	1	VE7_Hpv37

RESULT 1

ID	EPOR_HUMAN	STANDARD	PRT	508 AA.
AC	P19235			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Erythropoietin receptor precursor (EPO-R).			
GN	EPOR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91372359; PubMed=1654273;			
RA	Ennenman K., St John T.;			
RT	"The erythropoietin receptor gene: cloning and identification of			
RT	multiple transcripts in an erythroid cell line OCIM1.";			
RL	Exp. Hematol. 19:973-977(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90304340; PubMed=2163696;			
RA	Jones S.S., D'Andrea A.D., Haines L.L., Wong G.G.;			
RT	"Human erythropoietin receptor: cloning, expression, and biologic			
RT	characterization.";			
RL	Blood 76:31-35(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=92399733; PubMed=1668606;			
RA	Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N.,			
RA	Hankins W.D.;			
RT	"Cloning of the human erythropoietin receptor gene.";			
RL	Blood 78:2548-2556(1991).			
RN	[4]			
RP	SEQUENCE OF 1-96 FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=92399734; PubMed=1668607;			
RA	Maouche L., Tournamille C., Hattab C., Boffa G., Cartron J.-P.,			
RA	Chretien S.;			
RT	"Cloning of the gene encoding the human erythropoietin receptor.";			
RL	Blood 78:2557-2563(1991).			
RN	[5]			
RP	SEQUENCE OF 1-17 FROM N.A.			
RX	MEDLINE=92147143; PubMed=1664413;			
RA	Penny L.A., Forget B.G.;			
RT	"Genomic organization of the human erythropoietin receptor gene.";			
RL	Genomics 11:974-980(1991).			
RN	[6]			
RP	PHOSPHORYLATION, AND INTERACTION WITH APS.			
RX	MEDLINE=99301417; PubMed=10374881;			
RA	Wakioka T., Sasaki A., Mitsui K., Yokouchi M., Inoue A., Komiya S.,			
RA	Yoshimura A.;			
RT	"APS, an adaptor protein containing pleckstrin homology (PH) and Src			
RT	homology-2 (SH2) domains inhibits the JAK-STAT pathway in			

ALIGNMENTS

097b95 thermoplasm
P77161 escherichia
Q60041 thermotoga
Q9a2x6 caulobacter
O29265 archaeoglob
P38867 saccharomyc
P23760 homo sapien
P24610 mus musculu
P23759 homo sapien
P11141 caenorhabdi
O52225 thermus fil
P32670 escherichia

34 41 35.0 200 1 RS4_THEVO
35 41 35.0 292 1 GLXE_ECOLI
36 41 35.0 346 1 XYNE_THENE
37 41 35.0 413 1 PROA_CAUCR
38 41 35.0 416 1 Y997_ARCFU
39 41 35.0 452 1 YH7_YEAST
40 41 35.0 479 1 PAX3_HUMAN
41 41 35.0 479 1 PAX3_MOUSE
42 41 35.0 520 1 PAX7_HUMAN
43 41 35.0 657 1 HS7F_CABBL
44 41 35.0 833 1 DPOI_THEFI
45 41 35.0 833 1 PTIA_ECOLI

RT collaboration with c-Cbl.";

RL Leukemia 13:760-767(1999).

RN [7]

RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.

RA MEDLINE=96291992; PubMed=862530;

RA Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S.,

RA Wrighton N.C., Dover W.J., Jolliffe L.K., Wilson I.A.;

RT "Functional mimicry of a protein hormone by a peptide agonist: the

RT EPO receptor complex at 2.8 A.";

RL Science 273:464-471(1996).

RN [8]

RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.

RA MEDLINE=99023198; PubMed=9808045;

RA Livnah O., Johnson D.L., Stura E.A., Farrell F.X., Barbone F.P.,

RA You Y., Liu K.D., Goldsmith M.A., He W., Krause C.D., Pestka S.,

RA Jolliffe L.K., Wilson I.A.;

RT "An antagonist peptide-EPO receptor complex suggests that receptor

RT dimerization is not sufficient for activation.";

RL Nat. Struct. Biol. 5:993-1004(1998).

RN [9]

RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-244 IN COMPLEX WITH EPO.

RA MEDLINE=98445092; PubMed=9774108;

RA Syed R.S., Reid S.W., Li C., Cheatham J.C., Aoki K.H., Liu B.,

RA Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,

RA Elliott S., Sitney K., Katz B.A., Matthews D.J., Wendoloski J.J.,

RA Elgie J., Stroud R.M.;

RT "Efficiency of signalling through cytokine receptors depends

RT critically on receptor orientation.";

RL Nature 395:511-516(1998).

RN [10]

RX X-RAY CRYSTALLOGRAPHY (2.40 ANGSTROMS) OF 34-246.

RA MEDLINE=99141272; PubMed=9974392;

RA Livnah O., Stura E.A., Middleton S.A., Johnson D.L., Jolliffe L.K.,

RA Wilson I.A.;

RT "Crystallographic evidence for preformed dimers of erythropoietin

RT receptor before ligand activation.";

RL Science 283:987-990(1999).

CC -1- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-

CC induced erythroblast proliferation and differentiation. Upon EPO

CC stimulation, EPOR dimerizes triggering the JAK2/STAT5 signalling

CC cascade. Isoform 2 acts as a dominant-negative receptor of EPOR-

CC mediated signals.

CC -1- SUBUNIT: Interacts with APS.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.

CC Subfamily 1.

CC -1- SIMILARITY: Contains 1 fibronectin type III domain.

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CC -----

CC EMBL; M34986; AAA52401.1; -

CC EMBL; M60459; AAA52403.1; -

CC EMBL; S45332; AAB23271.1; -

CC EMBL; M76595; AAA52393.1; -

CC EMBL; M77244; AAA52392.1; -

CC PIR; A43799; ZUHUR.

CC PDB; 1EBP; 29-JUL-97.

CC PDB; 1EBA; 18-NOV-98.

CC PDB; 1EER; 01-OCT-99.

CC PDB; 1CNA; 11-AUG-99.

CC PDB; 1ERN; 07-JAN-00.

CC Genew; HGNC:3416; EPOR.

CC MIM; 133171; -

CC GO; GO:0005887; C:integral to plasma membrane; TAS.

CC GO; GO:0004900; F:erythropoietin receptor activity; TAS.

CC InterPro; IPR002996; CR1A.

CC InterPro; IPR008957; FN_III-like.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR003528; Hemtopoptn_L_F1.

DR Pfam; PF00041; fn3; 1.

DR PIRSF; PIRSF001959; EPO_receptor; 1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;

KW 3D-structure.

FT SIGNAL 1 24

FT CHAIN 25 508

FT DOMAIN 25 250

FT TRANSMEM 251 273

FT DOMAIN 274 508

FT DOMAIN 148 213

FT SITE 368 368

FT DISULFID 52 62

FT DISULFID 91 107

FT MOD_RES 368 368

FT CARBOHYD 76 76

FT HELIX 33 45

FT STRAND 51 54

FT STRAND 61 66

FT TURN 73 73

FT HELIX 74 76

FT STRAND 77 83

FT TURN 84 85

FT STRAND 89 90

FT STRAND 94 97

FT TURN 99 100

FT STRAND 103 108

FT HELIX 111 113

FT TURN 116 117

FT STRAND 120 126

FT TURN 127 128

FT STRAND 131 137

FT HELIX 139 141

FT STRAND 143 143

FT STRAND 149 155

FT STRAND 162 167

FT TURN 170 171

FT HELIX 175 177

FT STRAND 178 186

FT STRAND 195 198

FT TURN 200 201

FT STRAND 204 207

FT STRAND 215 224

FT TURN 226 228

FT STRAND 231 231

FT STRAND 240 243

SQ SEQUENCE 508 AA; 55065 MW; P9F326E162B9512A CRC64;

Query Match 100.0%; Score 117; DB 1; Length 508;

Best Local Similarity 100.0%; Pred. No. 8.3e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRVLEIGRTECVLSNLRGRTRY 23

DB 194 QRVLEIGRTECVLSNLRGRTRY 216

RESULT 2

EPOR MOUSE

ID EPOR MOUSE STANDARD; PRT; 507 AA.

AC P14753; O63852;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Erythropoietin receptor precursor (EPO-R).

GN EPOR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN SEQUENCE FROM N.A.
 RP MEDLINE=89195238; PubMed=2539263;
 RA D'Andrea A.D., Lodish H.F., Wong G.G.;
 RT "Expression cloning of the murine erythropoietin receptor.";
 RL Cell 57:277-285(1989).
 RN SEQUENCE FROM N.A.
 RP STRAIN=BALB/c; TISSUE=Liver;
 RC MEDLINE=91080149; PubMed=2175360;
 RA Kuramochi S., Ikawa Y., Todokoro K.;
 RT "Characterization of murine erythropoietin receptor genes.";
 RL J. Mol. Biol. 216:567-575(1990).
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92017832; PubMed=1656233;
 RA Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;
 RT "Unregulated expression of the erythropoietin receptor gene caused by
 RT insertion of spleen focus-forming virus long terminal repeat in a
 RT murine erythroleukemia cell line.";
 RL Mol. Cell. Biol. 11:5527-5533(1991).
 RN SEQUENCE OF 1-27 FROM N.A.
 RP MEDLINE=90287158; PubMed=2162479;
 RA Youssoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;
 RT "Structure and transcription of the mouse erythropoietin receptor
 RT gene.";
 RL Mol. Cell. Biol. 10:3675-3682(1990).
 RN SEQUENCE OF 1-24 FROM N.A.
 RP MEDLINE=91201346; PubMed=1849897;
 RA Lacombe C., Chretien S., Lemarchandel V., Mayeux P., Romeo P.H.,
 RA Gisselbrecht S., Cartron J.-P.;
 RT "Spleen focus-forming virus long terminal repeat insertional
 RT activation of the murine erythropoietin receptor gene in the T3C1-2
 RT friend leukemia cell line.";
 RL J. Biol. Chem. 266:6952-6956(1991).
 RN INTERACTION WITH APS.
 RP MEDLINE=93180826; PubMed=8382775;
 RA Miura O., Cleveland J.L., Ihle J.N.;
 RT "Inactivation of erythropoietin receptor function by point mutations
 RT in a region having homology with other cytokine receptors.";
 RL Mol. Cell. Biol. 13:1788-1795(1993).
 CC -1- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-
 CC induced erythroblast proliferation and differentiation. Upon EPO
 CC stimulation, EPOR dimerizes triggering the JAK2/STAT5 signaling
 CC cascade. Isoform 2 acts as a dominant-negative receptor of EPOR-
 CC mediated signals.
 CC -1- SUBUNIT: Interacts with APS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 1.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
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 DR EMBL; J04843; AAA37571.1; -.
 DR EMBL; X53081; CAA37248.1; -.

DR EMBL; M38133; AAA37572.1; -.
 DR EMBL; M62360; AAA37582.1; -.
 DR EMBL; S59388; AAB20029.2; -.
 DR PIR; A41686; A32385.
 DR PIR; S14081; S14081.
 DR HSSP; P19235; 1EBA.
 DR MGD; MGI:95408; EPOR.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003528; Hemopoetn_L_F1.
 DR Pfam; PF00441; fn3; 1.
 DR FIRSF; FIRSF001959; EPO_receptor; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01352; HEMATOPO REC L F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation.
 FT SIGNAL 1 24 ERYTHROPOIETIN RECEPTOR.
 FT CHAIN 25 507 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 25 249 POTENTIAL.
 FT TRANSMEM 250 272 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 273 507 FIBRONECTIN TYPE-III.
 FT DOMAIN 147 212 FIBRONECTIN TYPE-III.
 FT SITE 367 367 APS-BINDING (BY SIMILARITY).
 FT DISULFID 52 82 BY SIMILARITY.
 FT DISULFID 90 106 BY SIMILARITY.
 FT MOD RES 367 367 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 291 291 E -> D (IN REF. 3; AAB20029).
 SQ SEQUENCE 507 AA; 55194 MW; 067657A2E26451CA CRC64;
 Query Match 93.2%; Score 109; DB 1; Length 507;
 Best Local Similarity 91.3%; Pred. No. 1.5e-09;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QRVLELGTECVLSNLRGTRY 23
 DB 193 QRVLELGTECVLSNLRGTRY 215
 RESULT 3
 ID EPOR_RAT STANDARD; PRT; 507 AA.
 AC Q07303;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Erythropoietin receptor precursor (EPO-R).
 GN EPOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93366574; PubMed=7684373;
 RA Masuda S., Nagao M., Takahata K., Konishi Y., Gallyas F.,
 RA Tabira T., Sasaki R.;
 RT "Functional erythropoietin receptor of the cells with neural
 RT characteristics. Comparison with receptor properties of erythroid
 RT cells.";
 RL J. Biol. Chem. 268:11208-11216(1993).
 CC -1- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-
 CC induced erythroblast proliferation and differentiation. Upon EPO
 CC stimulation, EPOR dimerizes triggering the JAK2/STAT5 signaling
 CC cascade. Isoform 2 acts as a dominant-negative receptor of EPOR-
 CC mediated signals.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 1.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
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CC EMBL; D13566; BAA02761.1; -.
CC PIR; A46713; A46713.
CC HSSP; P19235; IEB.
CC InterPro; IPR002996; CR1A.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003528; Hemopoietin_L_F1.
CC Pfam; PF00041; fn3; 1.
CC PIRSF; PIRSF001959; EPO_receptor; 1.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS01352; HEMATOPO REC L_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24 BY SIMILARITY.
CC CHAIN 25 507 ERYTHROPOIETIN RECEPTOR.
CC DOMAIN 25 249 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 250 272 POTENTIAL.
CC DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 147 212 FIBRONECTIN TYPE-III.
CC DISULFID 52 62 BY SIMILARITY.
CC DISULFID 90 106 BY SIMILARITY.
CC CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 507 AA; AC79AF22D06A7312.CRC64;

Query Match 93.2%; Score 109; DB 1; Length 507;
Best Local Similarity 91.3%; Pred. No. 1.5e-09;
Matches 21; Conservative 1; Mismatches -1; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGTRY 23
DB 193 QRVLEIGRTECVLSNLRGGTRY 215

RESULT 4
GIDB_BIFLO STANDARD; PRT; 221 AA.
AC QG6J4; 20-0CT-2003 (Rel. 42, Created)
DT 10-0CT-2003 (Rel. 42, Last sequence update)
DT 10-0CT-2003 (Rel. 42, Last annotation update)
DE Methyltransferase gidB (EC 2.1.1.-) (Glucose inhibited division
DE protein B).
GN GIDB OR BL0646.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC 2705;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RA "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract".
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -1- FUNCTION: Probable S-adenosyl-L-methionine dependent
CC methyltransferase specific for a sterol and/or lipid substrate (By
CC similarity).
CC -1- SIMILARITY: Belongs to the gidB family.

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CC EMBL; AB014686; AAN24468.1; -.
CC HAMAP; MF_00074; -; 1.
CC InterPro; IPR003682; GidB.
CC Pfam; PF02527; GidB; 1.
CC ProDom; PD004441; GidB; 1.
CC TIGRFAMs; TIGR00138; gidB; 1.
CC Transferase; Methyltransferase; Complete proteome.

Query Match 41.9%; Score 49; DB 1; Length 221;
Best Local Similarity 45.0%; Pred. No. 1.8;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGR 20
DB 120 QNVLEIGRSDAVIQVRKR 139

RESULT 5
KRM1_MOUSE STANDARD; PRT; 473 AA.
ID KRM1_MOUSE
AC Q99N43; 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kremen protein 1 precursor (Kringles-containing protein marking the eye
DE and the nose) (Dickkopf receptor).
GN KREMEN1 OR KREMEN.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.; DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=21167372; PubMed=11267660;
RA Nakamura T., Aoki S., Kitajima K., Takahashi T., Matsumoto K.,
RA Nakamura T.;
RT "Molecular cloning and characterization of Kremen, a novel
RT kringles-containing transmembrane protein.";
RL Biochim. Biophys. Acta 1518:63-72(2001).
CC -1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
CC to block Wnt/beta-catenin signaling (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: In the adult, widely expressed with high
CC levels in heart, lung, kidney, skeletal muscle and testis.
CC -1- DEVELOPMENTAL STAGE: In the embryo, expression is first detected
CC on day 9 and increases up to day 18. Lower levels are found in
CC ectodermal ridge (AER) of the developing fore- and hindlimb buds,
CC the telencephalon and the first brachial arch. At 10.5 dpc,
CC expression is also observed in the myotome and in sensory tissues
CC such as the nasal pit and optic vesicle.
CC -1- SIMILARITY: Contains 1 CUB domain.
CC -1- SIMILARITY: Contains 1 kringles domain.
CC -1- SIMILARITY: Contains 1 WSC domain.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AB059617; BAB40968.1; -.
CC HSSP; P00747; 1CEA.
CC MGD; MGI:1933988; Kremen.
CC GO; GO:0016021; C:integral to membrane; NAS.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR000001; Kringles.

DR InterPro; IPR002889; WSC.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF0051; Kringlike; 1.
 DR Pfam; PF01822; WSC; 1.
 DR PRINTS; PR00018; Kringlike.
 DR ProDom; PD000395; Kringlike; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00021; Kringlike 1; 1.
 DR PROSITE; PS00070; Kringlike 2; 1.
 KW Wnt signaling pathway; Signal; Transmembrane; Kringlike.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 473 KREMEN PROTEIN 1.
 FT DOMAIN 21 392 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 393 413 POTENTIAL.
 FT DOMAIN 414 473 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 31 114 KRINGLE.
 FT DOMAIN 120 210 WSC.
 FT DOMAIN 214 321 CUB.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 473 AA; 51716 MW; 586827788BE3FDD1 CRC64;
 Query Match 41.9%; Score 49; DB 1; Length 473;
 Best Local Similarity 55.0%; Pred. No. 4.1;
 Matches 1; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 3 VEILEGRTECVLSNLRGRTR 22
 DB 268 VELLDDGYTHRVLSGRSR 287
 RESULT 6
 KRMI HUMAN
 ID KRMI HUMAN STANDARD; PRT; 475 AA.
 AC Q96M08; Q9BY70; Q9UGS5; Q9UGU1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kremen protein 1 precursor (Kringlike-containing protein marking the eye
 and the nose) (Dickkopf receptor).
 GN KREMEN1; OR KREMEN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Nakamura T., Nakamura T.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Okuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hiro Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
 RA Isegai T.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
 RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
 RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Dharmy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Evans K.L., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Gilbert J.G.R., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
 RA McAtyn J.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Suleston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Ioh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chiesoe S., Murray J., Miller N., Minx P.,
 RA Furlon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozeresky P., Rohlfing T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korfi J., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanaki J.P.,
 RA Peyrard M., Kedra D., Seroussi E., Fransson I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Sodenteich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tilahun Y., Wright H.;
 RT "The DNA sequence of human chromosome 22."
 RL Nature 402:489-495(1999).
 CC -1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
 to block Wnt/beta-catenin signaling (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q96M08-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q96M08-2; Sequence=VSP_003900;
 CC Note=No experimental confirmation available;
 CC -1- SIMILARITY: Contains 1 CUB domain.
 CC -1- SIMILARITY: Contains 1 kringlike domain.
 CC -1- SIMILARITY: Contains 1 WSC domain.
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 CC -----
 CC EMBL; AB059618; BAB40969.1; -
 CC EMBL; AK056425; BAB71180.1; -
 CC EMBL; Z95116; CAB62952.1; -
 CC EMBL; AL021393; CAB62959.1; -
 CC Genew; HGNC:17550; KREMEN1.
 CC GO; GO:0016021; C:integral to membrane; ISS.
 CC GO; GO:0005624; C:membrane fraction; TAS.
 CC GO; GO:0007154; P:cell communication; TAS.
 CC InterPro; IPR000859; CUB.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR002889; WSC.

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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:44:02 ; Search time 21 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: US-10-612-885a-1

Perfect score: 117

Sequence: 1 QRVLEGRTECVLSNLRGTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	100.0	508	1 ZUHUR	erythropoietin rec
2	109	93.2	265	2 S14081	erythropoietin rec
3	109	93.2	507	1 A2385	erythropoietin rec
4	109	93.2	507	1 A46713	erythropoietin rec
5	47	40.2	956	2 A57121	thrombospondin 3 p
6	46	39.3	67	2 S30006	ribosomal protein
7	46	39.3	67	2 S30005	probable DNA-bind
8	46	39.3	288	2 T30648	cytochrome P450 Rv
9	46	39.3	489	1 H70729	probable transcript
10	46	39.3	710	2 T41352	F4E2.4 protein -
11	46	39.3	1609	2 S44821	ATP-dependent RNA
12	45.5	38.9	607	1 S42639	probable transmem
13	45	38.5	316	2 D83406	hypothetical prote
14	45	38.5	512	1 D70506	axinin 1 precursor
15	45	38.5	1036	2 S22383	protein PV100 [imp
16	44.5	38.0	810	2 T44430	30S ribosomal prot
17	44	37.6	47	2 AB0673	hypothetical prote
18	44	37.6	195	2 AE1823	degenerate transpo
19	43	36.8	84	2 C97955	hypothetical prote
20	43	36.8	408	2 A87649	IS1167, transposas
21	43	36.8	418	2 C95184	IS1167, transposas
22	43	36.8	418	2 F95096	hypothetical prote
23	43	36.8	654	2 S76870	transferrin-bindin
24	43	36.8	931	2 S66574	thrombospondin 3 -
25	43	36.8	956	1 A46016	probable protein-t
26	43	36.8	1437	2 T31093	hypothetical prote
27	42.5	36.3	228	2 H71251	protein-tyrosine-p
28	42.5	36.3	1894	2 C54689	protein-tyrosine-p
29	42.5	36.3	1912	2 A56178	

ALIGNMENTS

RESULT 1

ZUHUR

erythropoietin receptor precursor - human

C/Species: Homo sapiens (man)

C/Date: 12-Feb-1993 #sequence revision 05-Apr-1995 #text change 22-Jun-1999

C/Accession: A43799; A60160; A49824; A53958; A53280; I52563

R/Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.

Blood 76, 31-35, 1990

A/Title: Human erythropoietin receptor: cloning, expression, and biologic characterizat

A/Reference number: A43799; MUID:90304340; PMID:2163696

A/Accession: A43799

A/Molecule type: mRNA

A/Residues: 1-508 <JON>

A/Cross-references: GB:M60459; NID:g182244; PIDN:AAA52403.1; PID:g182245

R/Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.

Blood 76, 24-30, 1990

A/Title: The gene for the human erythropoietin receptor: analysis of the coding sequence

A/Reference number: A60160; MUID:90304334; PMID:2163695

A/Accession: A60160

A/Status: not compared with conceptual translation

A/Molecule type: mRNA; DNA

A/Residues: 1-101, 'R', 103-188, 'RP', 191-243, 'E', 245-508 <WIN>

R/Nozuchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.

Blood 78, 2548-2556, 1991

A/Title: Cloning of the human erythropoietin receptor gene.

A/Reference number: A49824; MUID:92399733; PMID:1668606

A/Accession: A49824

A/Molecule type: DNA

A/Residues: 1-508 <NOG>

A/Cross-references: GB:S45332; NID:G255496; PIDN:AAB23271.1; PID:G255497

A/Experimental source: Placenta

A/Note: sequence extracted from NCBI backbone (NCBIN:113293, NCBIP:113294)

R/Ehrenman, K.; St. John, T.

Exp. Hematol. 19, 973-977, 1991

A/Title: The erythropoietin receptor gene: cloning and identification of multiple trans

A/Reference number: A53958; MUID:91372359; PMID:1654273

A/Accession: A53958

A/Molecule type: mRNA

A/Residues: 1-508 <EHR>

R/Penny, L.A.; Forget, B.G.

Genomics 11, 974-980, 1991

A/Title: Genomic organization of the human erythropoietin receptor gene.

A/Reference number: A55280; MUID:92147143; PMID:1664413

A/Accession: A55280

A/Molecule type: DNA

A/Residues: 1-17, 381-387, 'LLEQQODA', 391-395; 504-508 <PEN>

A/Note: sequence modified after extraction from NCBI backbone

A/Note: the authors translated the codon GAT for residue 31 as B

R/Maouche, L.; Tournamille, C.; Boffa, G.; Carttron, J.P.; Chretien, S.

Blood 78, 2557-2563, 1991

A/Title: Cloning of the gene encoding the human erythropoietin receptor.

A;Reference number: 152563; MUID:92399734; PMID:1668607
A;Accession: 152563
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-96 <RES>
A;Cross-references: GB:M76595; NID:g182147; PIDN:AAA52393.1; PID:g553281
C;Genetics:
A;Gene: GDB:EPOR
A;Cross-references: GDB:125242; OMIM:133171
A;Map position: 19p13.3-19p13.2
A;Introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
A;Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane protein
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-508/Product: erythropoietin receptor #status predicted <WAT>
F;52-508/Domain: extracellular #status predicted <EXT>
F;52-238/Domain: cytochrome receptor homology <CRS>
F;233-237/Region: WSXWS motif
F;231-272/Domain: transmembrane #status predicted <TMM>
F;273-508/Domain: intracellular #status predicted <INT>
F;52-62.91-107/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 117; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGTRY 23
|||||
Db 194 QRVLEGRTECVLSNLRGTRY 216
|||||

RESULT 2
S14081
erythropoietin receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S14081; 149653
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A;Title: Characterization of murine erythropoietin receptor genes.
A;Reference number: S13249; MUID:91080149; PMID:2175360
A;Accession: S14081
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 <KUR>
R;Lacombe, C.; Chretien, S.; Lemarchand, V.; Mayeux, P.; Romeo, P.
J. Biol. Chem. 266, 6952-6956, 1991
A;Title: Spleen focus-forming virus long terminal repeat insertional activation of the m
A;Reference number: 149653; MUID:91201346; PMID:1849897
A;Accession: 149653
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-24 <RES>
A;Cross-references: GB:M62360; NID:g193199; PIDN:AAA37562.1; PID:g193200
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: cytokine receptor; transmembrane protein
F;52-238/Domain: cytokine receptor homology <CRS>

Query Match 93.2%; Score 109; DB 2; Length 265;
Best Local Similarity 91.3%; Pred. No. 2.3e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGTRY 23
|||||
Db 193 QRVLEGRTECVLSNLRGTRY 215
|||||

RESULT 3
A32385
erythropoietin receptor precursor, membrane-bound form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999

C;Accession: A41686; A32385; S13249
R;Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A;Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
A;Reference number: A41686; MUID:92017832; PMID:1656233
A;Accession: A41686
A;Molecule type: mRNA
A;Residues: 1-507 <HIN>
A;Cross-references: GB:S59388; NID:g237036; PIDN:BA020029.1; PID:g237037
A;Experimental source: murine erythrocytopenia (MEL) cell line F5-5
R;D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989
A;Title: Expression cloning of the murine erythropoietin receptor.
A;Reference number: A32385; MUID:89195238; PMID:2539263
A;Accession: A32385
A;Molecule type: mRNA
A;Residues: 1-507 <DB>
A;Cross-references: GB:J04843; NID:g193090; PIDN:AAA37571.1; PID:g309219
A;Experimental source: murine erythrocytopenia (MEL) cells, subclone 745
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A;Title: Characterization of murine erythropoietin receptor genes.
A;Reference number: S13249; MUID:91080149; PMID:2175360
A;Accession: S13249
A;Molecule type: DNA; mRNA
A;Residues: 1-507 <KUR>
A;Cross-references: EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:g50862
A;Experimental source: murine erythrocytopenia K-1 cells
C;Genetics:
A;Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-507/Product: erythropoietin receptor #status predicted <WAT>
F;25-249/Domain: extracellular #status predicted <EXT>
F;250-271/Domain: cytochrome receptor homology <CRS>
F;272-507/Domain: transmembrane #status predicted <TMM>
F;52-62.90-106/Disulfide bonds: #status predicted <INT>
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.2%; Score 109; DB 1; Length 507;
Best Local Similarity 91.3%; Pred. No. 4.6e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGTRY 23
|||||
Db 193 QRVLEGRTECVLSNLRGTRY 215
|||||

RESULT 4
A46713
erythropoietin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A46713
R;Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasaki
J. Biol. Chem. 268, 11208-11216, 1993
A;Title: Functional erythropoietin receptor of the cells with neural characteristics. C
A;Reference number: A46713; MUID:93266574; PMID:7684373
A;Accession: A46713
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-507 <MAS>
A;Cross-references: GB:D13566; NID:g286209; PIDN:BA02761.1; PID:g286210
A;Experimental source: PC12 and erythroid cells
A;Note: sequence extracted from NCBI backbone (NCBI:132811, NCBI:132813)
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-507/Product: erythropoietin receptor #status predicted <WAT>
F;25-249/Domain: extracellular #status predicted <EXT>
F;52-238/Domain: cytokine receptor homology <CRS>

F;250-271/Domain: transmembrane #status predicted <TM>
F;272-507/Domain: intracellular #status predicted <INT>
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.2%; Score 109; DB 1; Length 507;
Best Local Similarity 91.3%; Pred. No. 4.6e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGRTY 23
|||:|||||:|||||:|||||
DB 193 QRVLEIGRTECVLSNLRGGTRY 215

RESULT 5

A57121
thrombospondin 3 precursor - human
C:Species: Homo sapiens (man)
C>Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C:Accession: A57121; T08830
R:Adolph, K.W.; Long, G.L.; Winfield, S.; Ginns, E.I.; Bornstein, P.
Genomics 27, 329-336, 1995
A:Title: Structure and organization of the human thrombospondin 3 gene (THBS3).
A:Reference number: A57121; MUID:9604440; PMID:7558000
A:Accession: A57121
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-956 <ADO>
R:Winfield, S.L.; Tayebi, N.; Martin, B.M.; Ginns, E.I.; Sidransky, E.
Genome Res. 7, 1020-1026, 1997
A:Title: Identification of three additional genes contiguous to the glucocerebrosidase 1
A:Reference number: Z16482; MUID:97474796; PMID:9331372
A:Accession: T08830
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-736 <WIN>
A:Cross-references: EMBL:AF023268; NID:92564910; PIDN:AAC51818.1; PID:g2564912
C:Genetics:
A:Gene: THBS3
A:Cross-references: GDB:409953; OMIM:188062
A:Map position: 1q21-1q23
A:Introns: 27/1; 96/1; 181/3; 216/1; 225/1; 256/1; 270/1; 319/3; 366/3; 392/3; 443/3; 48
C:Function:
A:Description: mediates cell-to-matrix and cell-to-cell interactions
C:Superfamily: thrombospondin 3; EGF homology
P:374-412/Domain: EGF homology <EGF>

Query Match 40.2%; Score 47; DB 2; Length 956;
Best Local Similarity 45.5%; Pred. No. 41;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGTR 22
|||:|||||:|||||:|||||
DB 113 QQGLADGKTHVLLRLGPR 134

RESULT 6

S30006
ribosomal protein S28.e - yeast (Kluyveromyces marxianus)
N:Alternate names: ribosomal protein YS33
C:Species: Kluyveromyces marxianus
C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999
C:Accession: S30006
R:Hoekstra, R.; Ferreira, P.M.; Booteman, T.C.; Mager, W.H.; Planta, R.J.
Yeast 8, 949-959, 1992
A:Title: Structure and expression of the ABF1-regulated ribosomal protein S33 gene in K1
A:Reference number: S30005; MUID:93127729; PMID:1481571
A:Accession: S30006
A:Molecule type: DNA
A:Residues: 1-67 <HOE>
A:Cross-references: GB:S52656
C:Genetics:
A:Gene: S33

C:Superfamily: rat ribosomal protein S28
C:Keywords: protein biosynthesis; ribosome

Query Match 39.3%; Score 46; DB 2; Length 67;
Best Local Similarity 42.9%; Pred. No. 3.7;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVEILEGRTECVLSNLRGTR 22
|||:|||||:|||||:|||||
DB 29 RVEFLEDTRTIVRNKGPVR 49

RESULT 7

S30005
ribosomal protein S28.e - yeast (Kluyveromyces marxianus var. lactis)
N:Alternate names: ribosomal protein YS33
C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999
C:Accession: S30005
R:Hoekstra, R.; Ferreira, P.M.; Booteman, T.C.; Mager, W.H.; Planta, R.J.
Yeast 8, 949-959, 1992
A:Title: Structure and expression of the ABF1-regulated ribosomal protein S33 gene in K1
A:Reference number: S30005; MUID:93127729; PMID:1481571
A:Accession: S30005
A:Molecule type: DNA
A:Residues: 1-67 <HOE>
A:Cross-references: GB:S53420
C:Genetics:
A:Gene: S33
C:Superfamily: rat ribosomal protein S28
C:Keywords: protein biosynthesis; ribosome

Query Match 39.3%; Score 46; DB 2; Length 67;
Best Local Similarity 42.9%; Pred. No. 3.7;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVEILEGRTECVLSNLRGTR 22
|||:|||||:|||||:|||||
DB 29 RVEFLEDTRTIVRNKGPVR 49

RESULT 8

T30648
probable DNA-binding protein 46L - Molluscum contagiosum virus 1
N:Alternate names: MC046L
C:Species: Molluscum contagiosum virus 1
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 27-Oct-2003
C:Accession: T30648
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A:Reference number: Z20876; MUID:96325459; PMID:8670425
A:Accession: T30648
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-288 <SEN>
A:Cross-references: EMBL:U60315; NID:91491943; PIDN:AAC55174.1; PID:91491989
C:Genetics:
A:Note: MC046L

C:Superfamily: DNA-binding phosphoprotein, vaccinia I3L type
C:Keywords: DNA binding

Query Match 39.3%; Score 46; DB 2; Length 288;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 ECVLNLRGTR 22
|||:|||||:|||||
DB 133 ECIVNLRGGTR 144

RESULT 9

H70729

A:Molecule type: DNA
A:Residues: 1-1609 <AND>
A:Cross-references: ENBL:L2646; NID:G388595; PID:G388601
C:Genetics:
A:Introns: 107/2; 173/2; 228/3; 594/3; 1165/2; 1216/3; 1231/3; 1258/2; 1300/2; 1321/3; 1
C:Superfamily: LDL receptor ligand-binding repeat homology
C:Fill-45/Domain: LDL receptor ligand-binding repeat homology <LDL>

Query Match 39.3%; Score 46; DB 2; Length 1609;
Best Local Similarity 66.7%; Pred. NO. 1e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 ILEGRTECVLSN 16
:|||||:|:
DB 877 LLEGRTECVWS 888

RESULT 12

S42639
ATP-dependent RNA helicase DB10 - wood tobacco
C:Species: Nicotiana sylvestris (wood tobacco)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C:Accession: S42639
R:Itadani, H.; Sugita, M.; Sugitara, M.
Plant Mol. Biol. 24, 249-252, 1994
A:Title: Structure and expression of a cDNA encoding an RNA helicase-like protein in tot
A:Reference number: S42639; MUID:94154240; PMID:8111024
A:Accession: S42639
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-607 <TA>
A:Cross-references: GB:D16247; NID:G465572; PIDN:BA003763.1; PID:G563986
C:Superfamily: tobacco ATP-dependent RNA helicase DB10; WW repeat homology
C:Keywords: ATP; nucleotide binding; P-loop
P:18-56/Domain: WW repeat homology <WW1>
P:189-196/Region: nucleotide-binding motif A (P-loop)
P:294-299/Region: nucleotide-binding motif B
P:298-301/Region: DEAD motif

Query Match 38.9%; Score 45.5; DB 1; Length 607;
Best Local Similarity 37.9%; Pred. NO. 44;
Matches 11; Conservative 4; Mismatches 5; Indels 9; Gaps 1;

QY 3 VEILEGRTECVLSNLR-----GRTR 22
:|||||:|:|:
DB 505 VKVLEGANQCVTELRDMASRGGMGRAR 533

RESULT 13

D83406
probable transmembrane sensor PA1911 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 28-Jul-2003
C:Accession: D83406
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B:
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83406
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-316 <STO>
A:Cross-references: GB:AE004617; GB:AE004091; NID:G9947901; PIDN:AA05299.1; GSPDB:GN00
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1911
C:Superfamily: Fe2+-dicitrate sensor, transmembrane component

Query Match 38.5%; Score 45; DB 2; Length 316;
Best Local Similarity 54.5%; Pred. NO. 27;
Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

```
7; Indels 0; Gaps 0;
```

7 EGRTECVLSNLRGRTRY 23
||| ||| : |||
296 EGYECEAEINIKGRDITY 312

Search completed: May 6, 2004, 12:47:27
Job time : 22 secs

QY	2	RVEILGRTECVLSNLRGRTRY	23
		: :	
Db	195	RVAVLAGRVE--LSPLHGRGRW	214

RESULT 14

D70506
hypothetical protein RV2733c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: D70506
R.V.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentile, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70506
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-512 <COL>
A:Cross-references: GB:Z98209; GB:AL123456; NID:G3261838; PIDN:CAB10909.1; PID:g2292967
A:Experimental source: strain H37RV
C:Genetic8:
A:Gene: RV2733c
C:Superfamily: conserved hypothetical protein b0835

Query Match	38.5%;	Score 45;	DB 1;	Length 512;
Best Local Similarity	42.3%;	Pred. No. 44;		
Matches 11;	Conservative 4;	Mismatches 7;	Indels 4;	Gaps 1;

Qy	1	Q	R	V	E	I	L	-----	E	G	R	T	E	C	V	L	S	N	L	R	G	T	R	22
Db	408	Q	A	V	E	L	V	A	T	G	E	G	R	K	D	T	T	A	R	M	S	G	R	433

RESULT 15
axinin 1 precursor - chicken
N:Alternate names: neural cell adhesion molecule AxCAM
C:Species: Gallus gallus (Chicken)
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: S22383, S34107; S69332; S2128
R:Zuellig, R.A.; Rader, C.; Schroeder, A.; Kalousek, M.B.; von Bohlen und Halbach, F.; C
Eur. J. Biochem. 204, 453-463, 1992
A:A:Title: The axonally secreted cell adhesion molecule, axinin-1. Primary structure, immu
A:Reference number: S22383; MUID:92174898; PMID:1311675
A:Accession: S22383
A:Molecule type: mRNA
A:Residues: 1-1036 <Zuellig>
A:Cross-references: EMBL:X63101; NID:G62852; PIDN:CAA44815.1; PID:G62853
A:Accession: S34107
A:Molecule type: protein
A:Residues: 29-49; 51-80; 84-95; 100-117; 120-128; 130-141; 143-176; 243-254; 256-296; 303-336; 333
R:R:Giger, R.J.; Vogt, L.; Zuellig, R.A.; Rader, C.; Henahan-Beatty, A.; Wolfer, D.P.; Son
Eur. J. Biochem. 227, 617-628, 1995
A:A:Title: The gene of chicken axinin-1. Complete structure and analysis of the promoter.
A:Reference number: S69332; MUID:95172044; PMID:7867620
A:Accession: S69332
A:A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1002-1036 <GIG>
A:Cross-references: EMBL:X79607
A:A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
C:Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C:Keywords: cell adhesion
P:1-23/Domain: signal sequence #status predicted <SIG>
P:24-1036/Product: axinin 1 #status predicted <MAT>
P:336-392/Domain: immunoglobulin homology <IMM>

Query Match 38.5%; Score 45; DB 2; Length 1036;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:38:56 ; Search time 54 Seconds
(without alignments)
120.344 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVLEIGRTECVLSNLGRTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	100.0	23	2 AAY39411	Human ery
2	117	100.0	23	5 AAU78011	Human ery
3	117	100.0	23	6 ABP72837	Erythro
4	117	100.0	30	2 AAR98938	Synthetic
5	117	100.0	211	3 AAB21686	Human mat
6	117	100.0	225	3 AAB21685	Human mat
7	117	100.0	438	3 AAY44622	Truncated
8	117	100.0	438	3 AAY44623	Truncated
9	117	100.0	458	7 ADE28671	Human NOV
10	117	100.0	458	7 ADE28673	Human NOV
11	117	100.0	458	7 ADE28675	Human NOV
12	117	100.0	488	2 AAW08349	EpoRfc fu
13	117	100.0	503	3 AAB13012	Q-tagged
14	117	100.0	508	2 AAR06512	EPO recep
15	117	100.0	508	2 AAR47518	Human EPO
16	117	100.0	508	2 AAR70032	Human ery
17	117	100.0	508	2 AAR69503	Human ery
18	117	100.0	508	5 ABB09173	Human ery
19	111	94.9	508	7 ADE28677	Human NOV
20	109	93.2	285	2 AAR50326	Mouse sol
21	109	93.2	507	2 AAR06511	EPO recep
22	109	93.2	507	2 AAR47517	MEL EPO r
23	109	93.2	507	2 AAR69502	Mouse ery
24	102	87.2	507	2 AAR50327	Mouse sol
25	54	44.4	1026	5 AAU80379	Human BIG

ALIGNMENTS

RESULT 1

AAU39411

ID AAY39411 standard; peptide; 23 AA.

XX AC AAY39411;

XX XX 30-NOV-1999 (first entry)

XX DE Human erythropoietin receptor-derived activation peptide.

XX KW Erythropoietin; EPO; receptor; activation; internalisation.

XX OS Synthetic.

XX OS Homo sapiens.

XX FN WO9942127-A2.

XX PD 26-AUG-1999.

XX PF 23-FEB-1999; 99WO-US003910.

XX PR 24-FEB-1998; 98US-00028938.

XX (RECE-) RECEPTRON INC.

XX PA Olsson L, Naranda T;

XX PI WPI; 1999-527422/44.

XX DR Modulating activity of type-2 cell surface receptors used in treatment of, e.g. obesity.

XX PT Claim 8; Page 17; 92pp; English.

XX PS This sequence represents a peptide derived from the extracellular activation sequence of the human erythropoietin (EPO) receptor.

XX CC Activation sequences are involved in modulation of receptor responses and are separate from the ligand binding site. Activation of receptor

XX CC important in two distinct ways: in the modulation of receptor

XX CC internalisation; and/or in the modulation of activation of the receptor.

XX CC Use of peptides corresponding to the activation sequence of a receptor

XX CC can retard or inhibit receptor internalisation, thereby increasing or

XX CC stabilising the steady-state number of active receptors on the cell

XX CC surface. This has the effect of increasing signalling per unit of ligand.

XX CC In addition, the receptor is classed as a type 2 cell surface receptor,

XX CC meaning that such peptides can actually replace the requirement for the

XX CC ligand, causing ligand-independent activation. This activation is

XX CC probably brought about by a dimerisation mechanism in which one peptide

CC molecule is bound by two receptors, mimicking the dimerisation and
CC subsequent activation that occurs when two receptors bind one ligand.
CC This peptide could be used to treat disorders involving an inadequate or
CC inappropriate response from its corresponding receptor

XX SQ Sequence 23 AA;
SQ Query Match 100.0%; Score 117; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0

QY 1 QRVLEIGRTECVLSNLRGRTRY 23
Db 1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 2
AAU78011 standard; peptide; 23 AA.
XX AAU78011;
AC AAU78011;
XX 05-JUN-2002 (first entry)
XX Human erythropoietin receptor activation domain oligopeptide.
XX Erythropoietin receptor; antidiabetic; activation sequence; ligand;
KW receptor internalisation; type 2 diabetes; drug screening; human.
XX Homo sapiens.
XX US6333031-B1.
PN 25-DEC-2001.
PD 24-FEB-1998; 98US-00028937.
XX 08-MAR-1996; 96US-00612999.
PR 22-AUG-1996; 96US-00701382.
PR 23-JAN-1997; 97US-00788820.
XX (RECE-) RECEPTRON INC.
XX Olsson L, Naranda T;
PI WPI; 2003-224899/28.
XX Composition comprising peptides from receptor extracellular domains,
PT useful for e.g. modulating receptor internalization and activation such
PT as increasing insulin activity.
XX Claim 1; Col 11; 48pp; English.
XX This invention corresponds to a novel composition comprising any of 34
CC peptides consisting of activation sequences from the extracellular
CC domains of cell-surface receptors. These peptides were identified by
CC homology searching with a peptide sequence from the MHC class I alpha 1
CC domain and correspond to the activation sequences of the associated
CC receptor. Activation sequences are involved in the internalisation of
CC receptors and so these peptides may be used to modulate the
CC internalisation and or activation of these receptors. The peptides of the
CC invention may also be used to increase effect of ligand signalling in
CC type 2 diabetes and can replace the ligand normally required for
CC activation. This is useful when the ligand is a hormone and is difficult
CC to obtain. The peptides may also interact synergistically with the ligand
CC or function as antagonists of receptor signalling. The peptides can also
CC be used in drug screening to identify compounds that modulate receptor
CC internalisation or function as ligand replacements. Use of these peptides
CC can increase the effect of therapeutic hormones (optionally co-
CC administered) by at least 50% and are specific for the receptors from
CC which they derive. The present sequence represents the human
CC Erythropoietin receptor activation sequence oligopeptide of the invention
XX

SQ Sequence 23 AA;
SQ Query Match 100.0%; Score 117; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0

QY 1 QRVLEIGRTECVLSNLRGRTRY 23
Db 1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 3
ABP72837 standard; peptide; 23 AA.
XX ABP72837;
AC ABP72837;
XX 11-AUG-2003 (first entry)
XX Erythropoietin mimetic peptide.
XX Transferrin; neuroprotective; cerebroprotective; vasotropic;
KW antiparkinsonian; nootropic; anti-HIV; antiasthmatic; anti-allergic;
KW cytostatic; immunosuppressive; antithrombotic; cardiant;
KW gynaecological; immunostimulant; antianaemic; haemostatic;
KW antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;
KW fungicide; hepatotropic; antirheumatic; antiarthritic; antigout;
KW tranquilizer; vulnerary; antidiabetic; nephrotropic; antipyretic;
KW gastrointestinal; gene therapy; transgenic animal; erythropoietin;
KW mimetic; agonist.
XX Synthetic.
OS WO2003020746-A1.
XX 13-MAR-2003.
XX 30-AUG-2002; 2002WO-US027637.
XX 30-AUG-2001; 2001US-0315745P.
PR 30-NOV-2001; 2001US-0334059P.
XX (BIOR-) BIOREXIS PHARM CORP.
XX Prior CP;
XX WPI; 2003-332916/31.
XX New fusion protein, useful in the diagnosis and treatment of diseases or
PT disorders relating to the respiratory, cardiovascular and digestive
PT systems, comprises a transferrin protein fused to a therapeutic protein.
XX Example 9; Page 255; 298pp; English.
XX The present sequence is that of an erythropoietin (EPO) mimetic peptide
CC which has no homology to natural EPO but has similar biological
CC properties in that it activates the EPO receptor acting as an agonist.
CC The EPO mimetic peptide can be included in novel fusion proteins of the
CC invention also including a transferrin (Tf, see ABP72820) moiety
CC engineered to extend the serum half-life or bioavailability. The EPO
CC mimetic peptide can be fused to the N- or C-terminus of Tf, or inserted
CC into, or used to replace part of Tf, such that the Tf acquires EPO
CC activity. Modified Tf fusion proteins of the invention can be used in the
CC diagnosis, prognosis, prevention and/or treatment of diseases and/or
CC disorders of the endocrine, nervous, immune, respiratory, cardiovascular,
CC reproductive and digestive systems, diseases and/or disorders relating to
CC the blood or to cell proliferation, inflammatory conditions and
CC infectious diseases, or to deliver a therapeutic agent to a cell or
CC across the blood-brain barrier
XX SQ Sequence 23 AA;
SQ Query Match 100.0%; Score 117; DB 6; Length 23;


```

Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGTRY 23
DB 1 QRVLEIGRTECVLSNLRGTRY 23

RESULT 4
AAR98938
ID AAR98938 standard; peptide; 30 AA.
XX AC AAR98938
XX DT 28-SEP-1996 (first entry)
XX DE Synthetic human erythropoietin receptor peptide, SE-8.
XX KW Monoclonal antibody; erythropoietin receptor; diagnosis; anaemia;
XX KW erythropoiesis; erythrocyte production; epitope mapping.
XX OS Synthetic.
XX PN WO9603438-A1.
XX PD 08-FEB-1996.
XX PP 26-JUL-1995; 95WO-US009458.
XX PR 26-JUL-1994; 94US-00280864.
XX PA (AMGE-) AMGEN INC.
XX PI Elliott SG;
XX DR WPI; 1996-117004/12.
XX PT Monoclonal antibodies stimulating an erythropoietin receptor - useful in
XX PT diagnosis and treatment of patients having disorders associated with low
XX PT red blood cell levels, e.g. anaemia.
XX PS Example 6; Page 34; 61pp; English.
XX CC AAR89960-R89965 and AAR98936-R98939 are overlapping, synthetic human
XX CC erythropoietin receptor (sHEPOR) peptides which span residues 1 to 244
XX CC of the human EPOR. The peptides are used to map the EPOR binding epitope
XX CC of an EPOR monoclonal antibody which binds to EPORs and stimulates
XX CC erythropoiesis by stimulating the proliferation and/or differentiation of
XX CC erythroid progenitor cells to erythrocytes. Pharmaceutical compans.
XX CC contg. the antibody may be used in the diagnosis and treatment of
XX CC patients having disorders associated with low red blood cell levels, e.g.
XX CC anaemia. The antibodies are also useful in methods and kits for detecting
XX CC EPORs in biological in biological samples
XX SQ Sequence 30 AA;

Query Match 100.0%; Score 117; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGTRY 23
DB 1 QRVLEIGRTECVLSNLRGTRY 23

RESULT 5
AAB21686
ID AAB21686 standard; peptide; 211 AA.
XX AC AAB21686
XX DT 21-DEC-2000 (first entry)
XX PA (XENC-) XENCOR INC.
XX XX

Human mature erythropoietin receptor EPOR extracellular domain #2.
Ligand; cell surface receptor; erythropoietin; EPOR; human;
protein design automation; PDA.
Homo sapiens.
WO200047612-A2.
17-AUG-2000.
11-FEB-2000; 2000WO-US003665.
11-FEB-1999; 99US-0120009P.
29-APR-1999; 99US-0131674P.
(XENC-) XENCOR INC.
Luo P, Dahiyat B;
WPI; 2000-549135/50.
Screening for ligand analogs and agents which modulate ligand-receptor
binding, comprises adding a test ligand to a non-naturally occurring cell
surface receptor analog.
Example 1; Fig 8; 82pp; English.
The present invention relates to a method for screening for a ligand
analog, comprising adding a candidate ligand to a non-naturally occurring
cell surface receptor analog e.g. erythropoietin receptor (sEPOR), and
determining the binding of the ligand to the analog. The present sequence
is a mature human erythropoietin receptor (EPOR) extracellular domain.
Protein Design Automation was carried out on the present sequence, so
that it may be used in the present invention as a cell surface receptor
analog
Sequence 211 AA;
Query Match 100.0%; Score 117; DB 3; Length 211;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTECVLSNLRGTRY 23
DB 161 QRVLEIGRTECVLSNLRGTRY 183

RESULT 6
AAB21685
ID AAB21685 standard; peptide; 225 AA.
XX AC AAB21685;
XX DT 21-DEC-2000 (first entry)
XX DE Human mature erythropoietin receptor EPOR extracellular domain #1.
XX KW Ligand; cell surface receptor; erythropoietin; EPOR; human.
XX OS Homo sapiens.
XX PN WO200047612-A2.
XX PD 17-AUG-2000.
XX PP 11-FEB-2000; 2000WO-US003665.
XX PR 11-FEB-1999; 99US-0120009P.
XX PR 29-APR-1999; 99US-0131674P.
XX PA (XENC-) XENCOR INC.
XX XX

```


new isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. rheumatoid arthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.

PR 17-APR-2002; 2002US-0373288P.
 PR 15-MAY-2002; 2002US-0380981P.
 PR 17-MAY-2002; 2002US-0381495P.
 PR 28-MAY-2002; 2002US-0383534P.
 PR 28-MAY-2002; 2002US-0383744P.
 PR 29-MAY-2002; 2002US-0383829P.
 PR 29-MAY-2002; 2002US-0384024P.
 PR 07-AUG-2002; 2002US-0401788P.
 PR 26-AUG-2002; 2002US-0406353P.
 PR 31-OCT-2002; 2002US-00287971.
 XX (CURA-) CURAGEN CORP.
 XX
 XX Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
 PI Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
 PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
 PI Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khrantsov NV;
 PI Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, McQueeney K;
 PI Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;
 PI Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shinkets RA;
 PI Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N;
 PI Vernet CAM, Zerhusen BD, Zhong M;
 XX WPI: 2003-441555/41.
 DR N-PSDB; ADE28672.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.
 XX
 PS Claim 1; SEQ ID NO 50; 447pp; English.
 XX
 CC The invention relates to a novel isolated NOVX polypeptide. The
 CC polypeptide of the invention demonstrates, antidiabetic, anorectic,
 CC cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial,
 CC fungicide, protozoacide, nootropic, neuroprotective, antiinflammatory,
 CC anticonvulsant, osteopathic, antiarthritic, antiinflammatory, cell
 CC dermatological, antiasthmatic and antilipemic activities. The
 CC polypeptides, nucleic acid molecules and antibodies may be useful for
 CC treating or diagnosing diseases including metabolic disorders such as
 CC diabetes and obesity, infectious diseases, anorexia, cancer,
 CC cardiovascular diseases including hypertension and atherosclerosis,
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's
 CC disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic
 CC disorders, inflammatory skin disorders, asthma and dyslipidaemia.
 CC Furthermore, the nucleic acids and polypeptides may also be used to
 CC identify molecules that modulate or inhibit neurogenesis, cell
 CC differentiation and proliferation, haemopoiesis, wound healing and
 CC angiogenesis, as well as in gene therapy. Finally, the nucleic acids may
 CC be used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV protein of the invention.
 XX
 SQ Sequence 458 AA;
 Query Match 100.0%; Score 117; DB 7; Length 458;
 Best Local Similarity 100.0%; Pred. NO. 1.1e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QRVLEIGRTECVLNLGRTRY 23
 DB 194 QRVLEIGRTECVLNLGRTRY 216
 RESULT 11
 ADE28675 standard; protein; 458 AA.
 XX
 XX ADE28675;
 AC
 XX
 DT 29-JAN-2004 (first entry)
 XX

DE Human NOV15c protein - SEQ ID 52.
 XX
 KW NOVX; antidiabetic; anorectic; cardiant; hypotensive;
 KW antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide;
 KW nootropic; neuroprotective; antiparkinsonian; anticonvulsant;
 KW osteopathic; antiarthritic; antiinflammatory; dermatological;
 KW antiasthmatic; antilipemic; metabolic; diabetes; obesity; infectious;
 KW anorexia; cancer; cardiovascular; hypertension; atherosclerosis;
 KW neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;
 KW osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;
 KW neurogenesis; cell differentiation; proliferation; haemopoiesis;
 KW wound healing; angiogenesis; gene therapy; chromosome mapping;
 KW tissue typing; human; NOV.
 XX
 XX Homo sapiens.
 OS
 XX WO2003040330-A2.
 XX
 XX 15-MAY-2003.
 PD
 XX 05-NOV-2002; 2002WO-US035536.
 PF
 XX 05-NOV-2001; 2001US-0338626P.
 PR 05-DEC-2001; 2001US-0336600P.
 PR 07-DEC-2001; 2001US-0338285P.
 PR 12-DEC-2001; 2001US-0341346P.
 PR 17-DEC-2001; 2001US-0341477P.
 PR 17-DEC-2001; 2001US-0341540P.
 PR 20-DEC-2001; 2001US-0342592P.
 PR 27-DEC-2001; 2001US-0344297P.
 PR 31-DEC-2001; 2001US-0344903P.
 PR 17-APR-2002; 2002US-0373288P.
 PR 15-MAY-2002; 2002US-0380981P.
 PR 17-MAY-2002; 2002US-0381495P.
 PR 28-MAY-2002; 2002US-0383534P.
 PR 28-MAY-2002; 2002US-0383744P.
 PR 29-MAY-2002; 2002US-0383829P.
 PR 29-MAY-2002; 2002US-0384024P.
 PR 07-AUG-2002; 2002US-0401788P.
 PR 26-AUG-2002; 2002US-0406353P.
 PR 31-OCT-2002; 2002US-00287971.
 XX (CURA-) CURAGEN CORP.
 XX
 XX Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
 PI Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
 PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
 PI Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khrantsov NV;
 PI Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, McQueeney K;
 PI Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;
 PI Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shinkets RA;
 PI Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N;
 PI Vernet CAM, Zerhusen BD, Zhong M;
 XX WPI: 2003-441555/41.
 DR N-PSDB; ADE28674.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.
 XX
 PS Claim 1; SEQ ID NO 52; 447pp; English.
 XX
 CC The invention relates to a novel isolated NOVX polypeptide. The
 CC polypeptide of the invention demonstrates, antidiabetic, anorectic,
 CC cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial,
 CC fungicide, protozoacide, nootropic, neuroprotective, antiinflammatory,
 CC anticonvulsant, osteopathic, antiarthritic, antiinflammatory, cell
 CC dermatological, antiasthmatic and antilipemic activities. The
 CC polypeptides, nucleic acid molecules and antibodies may be useful for
 CC treating or diagnosing diseases including metabolic disorders such as
 CC diabetes and obesity, infectious diseases, anorexia, cancer,
 CC cardiovascular diseases including hypertension and atherosclerosis,
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's
 CC disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic
 CC disorders, inflammatory skin disorders, asthma and dyslipidaemia.
 CC Furthermore, the nucleic acids and polypeptides may also be used to
 CC identify molecules that modulate or inhibit neurogenesis, cell
 CC differentiation and proliferation, haemopoiesis, wound healing and
 CC angiogenesis, as well as in gene therapy. Finally, the nucleic acids may
 CC be used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV protein of the invention.
 XX

CC cardiovascular diseases including hypertension and atherosclerosis,
CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's
CC disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic
CC disorders, inflammatory skin disorders, asthma and dyslipidaemia.
CC Furthermore, the nucleic acids and polypeptides may also be used to
CC identify molecules that modulate or inhibit neurogenesis, cell
CC differentiation and proliferation, haemopoiesis, wound healing and
CC angiogenesis, as well as in gene therapy. Finally, the nucleic acids may
CC be used as hybridisation probes, in chromosome mapping, tissue typing,
CC preventive medicine and pharmacogenomics. The current sequence is that of
CC the human NOV protein of the invention.

XX
XX
SQ Sequence 458 AA;

Query Match 100.0%; Score 117; DB 7; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLRGTRY 23
Db 194 QRVLEIGRTECVLSNLRGTRY 216

RESULT 12
AAW08349
ID AAW08349 standard; protein; 488 AA.
XX
AC AAW08349;
DT 14-MAR-1997 (first entry)
XX
XX
DE EpoRfc fusion protein.
XX
XX Receptor agonist; antibody; erythropoietin receptor; EpoR; immunogen;
KW antigen; metallothionein; promoter; IgG1; Fc; anaemia; therapy.
XX
XX Homo; sapiens.
OS Synthetic.
OS Chimeric.
XX
XX
FH Key Location/Qualifiers
FT Domain 1. .250
FT /label= EpoR-ECD
FT /note= "erythropoietin receptor extracellular domain"
FT Cleavage-site 251. .254
FT /note= "Factor Xa cleavage site"
FT Domain 255. .488
FT /label= Fc
FT /note= "human IgG1 Fc sequence"

XX WO9640231-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009613.
XX
XX 07-JUN-1995; 95US-00474673.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Young PR, Erickson-Miller CL;
XX
XX WPI; 1997-051900/05.
XX N-PSDB; AAT48800.
XX
XX Recombinant immunogen corresp. to dimeric form of a receptor - used for
PT generating antibodies able to act as receptor agonists, esp. of
PT erythropoietin receptor for treating anaemia.
XX
XX Example 1; Page 39-41; 83pp; English.
XX
XX A fusion protein (AAW08349) encoded by plasmid mtaIsEpoRfc (AAT48800)
CC comprises the human erythropoietin receptor (EpoR) extracellular domain

CC fused (via a Factor Xa cleavage sequence) to the Fc portion of human
CC IgG1. It can be expressed e.g. in transfected Drosophila S2 cells upon
CC induction with copper sulphate. The cells secrete EpoRfc as a dimeric
CC molecule due to the affinity of the Fc moiety for itself. The dimeric
CC receptor can be used as an immunogen to generate antibodies (monoclonal,
CC polyclonal, chimeric, humanised) able to act as EpoR agonists for use in
CC treatment of anaemia

XX
XX
SQ Sequence 488 AA;

Query Match 100.0%; Score 117; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLRGTRY 23
Db 194 QRVLEIGRTECVLSNLRGTRY 216

RESULT 13
AAB13012
ID AAB13012 standard; protein; 503 AA.
XX
AC AAB13012;
XX
DT 08-DEC-2000 (first entry)
XX
XX Q-tagged erythropoietin (EPO) receptor protein.
XX
XX Site specific label; detection; interaction screening; transglutaminase;
KW erythropoietin receptor; EPO.
XX
XX Synthetic.
XX
XX WO200043492-A2.
XX
XX 27-JUL-2000.
XX
XX 20-JAN-2000; 2000WO-US001481.
XX
XX 22-JAN-1999; 99US-0117327P.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Tew DG, Powell DJ, Meek TD, Chen W;
XX
XX WPI; 2000-499222/44.

XX
XX Screening for a candidate compound for use in bioassays comprises
PT contacting the candidate molecule with a labelled modified protein and
PT detecting the label to identify interaction of the two molecules.
XX
XX Example 4; Page 26; 49pp; English.
XX
XX This invention relates to methods for the site specific modification of a
CC protein, and to a method for screening for a candidate compound which
CC interacts with first protein. The screening method comprises contacting
CC the candidate molecule with a labelled modified first protein and
CC detecting the label to identify interaction of the labelled modified
CC first protein and candidate compound. The first protein is modified to
CC contain a peptide, represented by sequence AAB13005. The method is used
CC to label proteins at specific sites. The present sequence represents a Q-
CC tagged erythropoietin (EPO) receptor constructed in an example of the
CC method of the invention

XX
XX
SQ Sequence 503 AA;

Query Match 100.0%; Score 117; DB 3; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLRGTRY 23

Db 194 QRVLEGRTECVLSNLRGTRY 216

RESULT 14
AAR06512 standard; protein; 508 AA.

XX AAR06512
AC AAR06512
XX 25-MAR-2003 (revised)
DT 04-JAN-1991 (first entry)
XX
DE EPO receptor.
XX
XX Erythropoietin; Diamond Blackfan anaemia; polycythemia vera.
KW
XX Homo sapiens.
OS
XX W09008822-A.
FN
XX 09-AUG-1990.
PD
XX 03-FEB-1989; 89US-00306503.
PF
XX 03-FEB-1989; 89US-00306503.
PR
XX (GEMY) GENETICS INST INC.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Dandrea A, Wong G;
PI
XX WPI; 1990-260931/34.
DR
XX N-PSDB; AAQ05748.
DR
XX Erythropoietin receptor and gene - used for developing reagents and systems to control and study erythropoiesis.
PT
XX Disclosure; Fig 2; 53pp; English.
PS
XX The sequence was deduced from DNA obtd. from a clone isolated from a commercially available human genomic cDNA library in phage Lambda Fix (Stratagene). The sequence encodes a type I trans- membrane protein with binding affinity for EPO. The gene and recombinant EPO receptor produced on expression of the DNA are used to develop reagents and systems to control and study erythropoiesis. It is believed that the EPO receptor is dys- functional in individuals with Diamond Blackfan anaemia, and may be hyperactive in polycythemia vera. See also AAR06511 (murine EPO receptor). (Updated on 25-MAR-2003 to correct PI field.)
CC
XX MAR-2003 to correct PI field.)
CC
XX Sequence 508 AA;
SQ

Query Match 100.0%; Score 117; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGTRY 23
Db 194 QRVLEGRTECVLSNLRGTRY 216

RESULT 15
AAR47518 standard; protein; 508 AA.
ID
XX AAR47518
AC
XX
XX 25-MAR-2003 (revised)
DT 24-JUN-1994 (first entry)
XX
XX Human EPO receptor.
DE
XX Erythropoietin receptor; recombinant; murine; anaemia.
KW

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT /note= "signal peptide"
XX FT Protein 25..508
XX FT /note= "mature EPO receptor"
XX FT Region 251..272
XX FT /note= "putative transmembrane domain"
XX
XX US5278065-A.
FN
XX 11-JAN-1994.
PD
XX 25-MAR-1991; 91US-00678877.
PF
XX 03-FEB-1989; 89US-00306503.
PR
XX (GEMY) GENETICS INST INC.
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX D'andrea A, Wong GG, Jones SS;
PI
XX WPI; 1994-025409/03.
DR
XX N-PSDB; AAQ53995.
DR
XX Recombinant DNA encoding erythropoietin receptor - used to develop prods. for study, treatment or diagnosis of disorders in which receptor is dysfunctional.
PT
XX Disclosure; Fig 9; 24pp; English.
PS
XX Mouse erythroleukaemia (MEL) cells were used to construct a cDNA library. The cDNA was used to transfect COS-1 cells and these were screened for radioiodinated erythropoietin (EPO) binding to isolate cDNA encoding the EPO receptor. This cDNA was used as a probe to screen a human genomic cDNA library to obtain DNA encoding the human EPO receptor. The cDNA may be used to study, treat or diagnose disorders in which the EPO receptor is dysfunctional. The EPO receptor may also be used to raise antibodies or for treating hypersensitivity to EPO or who have elevated levels of EPO. The prod. is pref. used for treating anaemias, primary proliferative polycythemia and secondary polycythemia. See also AAR47517. (Updated on 25-MAR-2003 to correct PF field.)
CC
XX Sequence 508 AA;
SQ

Query Match 100.0%; Score 117; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGTRY 23
Db 194 QRVLEGRTECVLSNLRGTRY 216

Search completed: May 6, 2004, 12:45:02
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:42:22 ; Search time 23 Seconds
(without alignments)
51.626 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVLEIGRTECVLSNLRGRTRY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA:*

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	100.0	23	4	US-09-028-937-11
2	117	100.0	30	2	US-08-280-864A-12
3	117	100.0	30	4	US-09-092-291-12
4	117	100.0	438	4	US-09-339-838-5
5	117	100.0	438	4	US-09-339-838-7
6	117	100.0	488	3	US-08-776-511-2
7	117	100.0	508	2	US-08-850-293-5
8	49	41.9	321	3	US-09-039-609-4
9	49	41.9	458	3	US-09-039-609-2
10	46	39.3	64	4	US-09-134-000C-5287
11	46	39.3	67	4	US-09-732-210-1599
12	46	39.3	67	4	US-09-732-210-1500
13	45	38.5	372	4	US-09-252-991A-32067
14	44	37.6	493	4	US-09-489-039A-12903
15	43	36.8	931	4	US-08-624-655A-2
16	42	35.9	67	4	US-09-732-210-1601
17	42	35.9	252	4	US-09-252-991A-32222
18	42	35.9	283	4	US-08-956-171E-5203
19	42	35.9	363	4	US-09-134-000C-3764
20	42	35.9	605	2	US-08-752-307B-8
21	42	35.9	605	4	US-09-707-802-8
22	42	35.9	605	4	US-09-991-326-8
23	42	35.9	623	4	US-09-252-991A-23930
24	42	35.9	1018	1	US-08-452-052-2
25	42	35.9	1101	3	US-08-986-485-2
26	42	35.9	1611	2	US-08-804-227C-5
27	42	35.9	3729	2	US-08-804-227C-4

Sequence 2, Appli
Sequence 14, Appli
Sequence 621, Ap
Sequence 14, Appli
Sequence 15, Appli
Sequence 13, Appli
Sequence 438, App
Sequence 435, Ap
Sequence 1731, A
Sequence 155, App
Sequence 243, App
Sequence 7545, Ap
Sequence 20894, A
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli

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29 42 35.9 4545 2 US-08-804-227C-14
30 41 35.0 50 4 US-09-621-976-612
31 41 35.0 60 4 US-08-754-477A-14
32 41 35.0 60 4 US-08-754-477A-15
33 41 35.0 75 3 US-08-928-383B-13
34 41 35.0 292 4 US-09-711-164-438
35 41 35.0 327 4 US-09-134-001C-3535
36 41 35.0 749 4 US-09-252-991A-17331
37 41 35.0 835 4 US-09-758-282B-155
38 41 35.0 835 4 US-09-758-282B-243
39 41 35.0 843 4 US-09-489-039A-7545
40 41 35.0 865 4 US-09-252-991A-20894
41 41 35.0 1018 1 US-08-408-093-6
42 41 35.0 1018 1 US-08-408-420A-6
43 41 35.0 1018 1 US-08-714-901-6
44 41 35.0 1018 3 US-08-040-741-6
45 41 35.0 1091 3 US-08-986-485-5

ALIGNMENTS

RESULT 1
US-09-028-937-11
; Sequence 11, Application US/09028937
; Patent No 6333031
; GENERAL INFORMATION:
; APPLICANT: Olsson, Lennart
; APPLICANT: Naranda, Tatjana
; TITLE OF INVENTION: Receptor Derived Peptides As Modulators
; TITLE OF INVENTION: Of Receptor Activity
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Holbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/028,937
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/788,820
; FILING DATE: 23-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/701,382
; FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/612,999
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 949-8711
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-028-937-11

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,291
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280864
FILING DATE: 25-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-307A
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-092-291-12

Query Match 100.0%; Score 117; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTRY 23
DB 1 QRVLEGRTECVLSNLRGRTRY 23

Query Match 100.0%; Score 117; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTRY 23
DB 1 QRVLEGRTECVLSNLRGRTRY 23

RESULT 4
US-09-339-838-5
Sequence 5, Application US/09339838
Patent No. 6361998
GENERAL INFORMATION:
APPLICANT: Bell, David N.
APPLICANT: Mueller, Susan G.
APPLICANT: Matthews, Kathryn E.
TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemog
FILE REFERENCE: 6704-83
CURRENT APPLICATION NUMBER: US/09/339,838
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: CA 2,260,332
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: CA 2,241,576
PRIOR FILING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 438
TYPE: PRT
ORGANISM: Homo sapiens
US-09-339-838-5

Query Match 100.0%; Score 117; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTRY 23
DB 194 QRVLEGRTECVLSNLRGRTRY 216

RESULT 5
US-09-339-838-7
Sequence 7, Application US/09339838
Patent No. 6361998
GENERAL INFORMATION:
APPLICANT: Bell, David N.
APPLICANT: Mueller, Susan G.
APPLICANT: Matthews, Kathryn E.

Query Match 100.0%; Score 117; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTRY 23
DB 1 QRVLEGRTECVLSNLRGRTRY 23

RESULT 2
US-08-280-864A-12
Sequence 12, Application US/08280864A
Patent No. 585574
GENERAL INFORMATION:
APPLICANT: Elliott, Steven G.
TITLE OF INVENTION: Antibodies Which Activate an
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Behavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.A.
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,864A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-307
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-280-864A-12

Query Match 100.0%; Score 117; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTRY 23
DB 1 QRVLEGRTECVLSNLRGRTRY 23

RESULT 3
US-09-092-291-12
Sequence 12, Application US/09092291
Patent No. 6319499
GENERAL INFORMATION:
APPLICANT: Elliott, Steven G.
TITLE OF INVENTION: Antibodies Which Activate an
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.A.
ZIP: 91320
COMPUTER READABLE FORM:

;; TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemoglo
;; FILE REFERENCE: 6704-83
;; CURRENT APPLICATION NUMBER: US/09/339,838
;; CURRENT FILING DATE: 1999-06-25
;; PRIOR APPLICATION NUMBER: CA 2,260,332
;; PRIOR FILING DATE: 1999-01-25
;; PRIOR APPLICATION NUMBER: CA 2,241,576
;; PRIOR FILING DATE: 1998-06-25
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 7
;; LENGTH: 438
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-339-838-7

Query Match 100.0%; Score 117; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVILEGRTECVLSNLRGRTRY 23
Db 194 QRVILEGRTECVLSNLRGRTRY 216

RESULT 6
US-08-776-511-2
;; Sequence 2, Application US/08776511
;; Patent No. 6153190
;; GENERAL INFORMATION:
;; APPLICANT: Young, Peter R.
;; APPLICANT: Erickson-Miller, Connie
;; TITLE OF INVENTION: Method for Obtaining Receptor Agonist
;; TITLE OF INVENTION: Antibodies
;; NUMBER OF SEQUENCES: 13
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corporation- Corporate
;; ADDRESSEE: Patents
;; STREET: 709 Swedeland Road
;; CITY: King of Prussia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19406-2799
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/776,511
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jervis, Herbert H.
;; REGISTRATION NUMBER: 31,171
;; REFERENCE/DOCKET NUMBER: SPC P50349-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5015
;; TELEFAX: 610-270-5030
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 488 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-776-511-2

Query Match 100.0%; Score 117; DB 3; Length 488;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVILEGRTECVLSNLRGRTRY 23
Db 194 QRVILEGRTECVLSNLRGRTRY 216

RESULT 7
US-08-850-293-5
;; Sequence 5, Application US/08850293
;; Patent No. 5843726
;; GENERAL INFORMATION:
;; APPLICANT: Lee, Jong Y.
;; TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
;; TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C., P.A.
;; STREET: 60 South Sixth Street, Suite 3300
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/850,293
;; FILING DATE: 05-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/499,643
;; FILING DATE: 07-JUL-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/106,815
;; FILING DATE: 16-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ellinger, Mark S.
;; REGISTRATION NUMBER: 34,812
;; REFERENCE/DOCKET NUMBER: 07004/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612/335-5070
;; TELEFAX: 612/288-9696
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 508 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-850-293-5

Query Match 100.0%; Score 117; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVILEGRTECVLSNLRGRTRY 23
Db 194 QRVILEGRTECVLSNLRGRTRY 216

RESULT 8
US-09-039-609-4
;; Sequence 4, Application US/09039609
;; Patent No. 6107473
;; GENERAL INFORMATION:
;; APPLICANT: ALBONE, EARL
;; APPLICANT: KIKLY, KRISTINE
;; TITLE OF INVENTION: A KRINGLE-RELATED CLONE,
;; TITLE OF INVENTION: HTHB247
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ratner & Prestia
;; STREET: P.O. Box 980
;; CITY: Valley Forge
;; STATE: PA

QY 2 RVEILGRTTCVLSNLRGRTRY 23
Db 251 RVAVLGRVE--LSPLHGRGW 270

RESULT 14
US-09-489-039A-12903
; Sequence 12903, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12903
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12903

Query Match 37.6%; Score 44; DB 4; Length 493;
Best Local Similarity 45.0%; Pred. No. 45;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 4 EILEGRTTCVLSNLRGRTRY 23
Db 111 EALEGKTFCVRKRGKHEF 130

RESULT 15
US-08-624-655A-2
; Sequence 2, Application US/08624655A
; Patent No. 6323005
; GENERAL INFORMATION:
; APPLICANT: DABAN, MONTERRAT
; APPLICANT: MEDRANO, ANDRES
; APPLICANT: ESPUNA, ENRIC
; APPLICANT: QUEROL, ENRIQUE
; TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEIN 1 (Tbpl) GENE OF
; TITLE OF INVENTION: Actinobacillus pleuropneumoniae, ITS USE TO PREPARE
; TITLE OF INVENTION: PRODUCTS FOR THE UTILIZATION IN VACCINES FOR
; TITLE OF INVENTION: PLEUROPNEMONIA AND AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: P00740
; CURRENT APPLICATION NUMBER: US/08/624,655A
; CURRENT FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: 95 00592
; PRIOR FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-08-624-655A-2

Query Match 36.8%; Score 43; DB 4; Length 931;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 6 LEGRTECVLSNLRGRTRY 23
Db 581 IAGRADCATSKIRGHNY 598

Search completed: May 6, 2004, 12:46:53
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QY 2 RVEILGRTTCVLSNLRGRTR 22
Db 29 RVEFLEDTTIVRVKGPVR 49

RESULT 12
US-09-732-210-1600
; Sequence 1600, Application US/09732210
; Patent No. 8573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1600
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Kluyveromyces marxianus
US-09-732-210-1600

Query Match 39.3%; Score 46; DB 4; Length 67;
Best Local Similarity 42.9%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVEILGRTTCVLSNLRGRTR 22
Db 29 RVEFLEDTTIVRVKGPVR 49

RESULT 13
US-09-252-991A-32067
; Sequence 32067, Application US/09252991A
; Patent No. 8551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32067
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32067

Query Match 38.5%; Score 45; DB 4; Length 372;
Best Local Similarity 54.5%; Pred. No. 22;
Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVLEIGRTECVLSNLGRTRY 23

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	117	100.0	23	16	US-10-231-494-30
3	117	100.0	30	15	US-10-364-276-12
4	117	100.0	458	12	US-10-287-971-48
5	117	100.0	458	12	US-10-287-971-50
6	117	100.0	458	12	US-10-287-971-52
7	117	100.0	508	9	US-09-016-159-5
8	115	96.6	508	12	US-10-287-971-54
9	105	88.0	109	15	US-10-316-194-142
10	95	82.1	109	15	US-10-316-194-144
11	93	79.5	109	15	US-10-316-194-35
12	86	73.5	109	15	US-10-316-194-43
13	52	44.4	1026	10	US-09-947-063-4
14	52	44.4	1026	10	US-09-947-063-11
15	45	41.9	49	9	US-09-728-912-7

16	49	41.9	110	14	US-10-029-386-27439	Sequence 27439, A
17	49	41.9	341	9	US-09-848-288-4	Sequence 4, Appli
18	49	41.9	373	10	US-09-759-1308-376	Sequence 376, App
19	49	41.9	373	13	US-10-042-431-6	Sequence 6, Appli
20	49	41.9	413	9	US-09-728-912-2	Sequence 2, Appli
21	49	41.9	451	10	US-09-759-1308-413	Sequence 413, App
22	49	41.9	451	13	US-10-042-431-43	Sequence 43, Appl
23	49	41.9	456	10	US-09-759-1308-375	Sequence 375, App
24	49	41.9	456	13	US-10-042-431-5	Sequence 5, Appli
25	49	41.9	458	16	US-10-467-042-16	Sequence 16, Appl
26	49	41.9	470	10	US-09-759-1308-439	Sequence 439, App
27	49	41.9	470	13	US-10-042-431-69	Sequence 69, Appl
28	49	41.9	475	10	US-09-759-1308-373	Sequence 373, App
29	49	41.9	475	13	US-10-042-431-3	Sequence 3, Appli
30	49	41.9	492	15	US-10-094-749-2546	Sequence 2546, Ap
31	48	41.0	312	9	US-09-738-626-5282	Sequence 5282, Ap
32	47.5	40.6	419	15	US-10-369-493-9725	Sequence 9725, Ap
33	47	40.2	85	14	US-10-029-386-32900	Sequence 32900, A
34	47	40.2	191	12	US-10-424-599-181458	Sequence 181458,
35	47	40.2	386	12	US-10-424-599-181457	Sequence 181457,
36	46	39.3	494	12	US-10-425-114-50005	Sequence 50005, A
37	46	39.3	941	12	US-10-425-114-72012	Sequence 72012, A
38	45	38.5	686	15	US-10-162-335-46	Sequence 46, Appl
39	45	38.5	686	15	US-10-162-335-48	Sequence 48, Appl
40	45	38.5	686	15	US-10-162-335-50	Sequence 50, Appl
41	45	38.5	686	15	US-10-162-335-52	Sequence 52, Appl
42	45	38.5	961	15	US-10-162-335-42	Sequence 42, Appl
43	44	37.6	87	12	US-10-424-599-196538	Sequence 196538,
44	44	37.6	250	12	US-10-424-599-236053	Sequence 236053,
45	44	37.6	873	12	US-10-425-114-65968	Sequence 65968, A

ALIGNMENTS

RESULT 1

US-09-991-548-11
; Sequence 11, Application US/09991548.
; Patent No. US20020160013A1
; GENERAL INFORMATION:
; APPLICANT: OLSSON, Lennart
; APPLICANT: NARANDA, Tatjana
; TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES AS MODULATORS
; TITLE OF INVENTION: OF RECEPTOR ACTIVITY
; FILE REFERENCE: 213542000101
; CURRENT APPLICATION NUMBER: US/09/991,548
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/028,937
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 08/788,820
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/701,382
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: 08/612,999
; PRIOR FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human erythropoietin receptor
US-09-991-548-11

Query Match 100.0%; Score 117; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 QRVLEIGRTECVLSNLGRTRY 23

Db 1 QRVLEIGRTECVLSNLGRTRY 23

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RESULT 2
US-10-231-494-30
; Sequence 30, Application US/10231494
; Publication No. US2004002334A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
US-10-231-494-30

Query Match      100.0%; Score 117; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23
Db 1 QRVLEIGRTECVLSNLGRTRY 23

RESULT 3
US-10-364-276-12
; Sequence 12, Application US/10364276
; Publication No. US2003021544A1
; GENERAL INFORMATION:
; APPLICANT: Eliott, Steven G
; TITLE OF INVENTION: Antibodies which Activate an Erythropoietin Receptor
; FILE REFERENCE: 06843-0030-04000
; CURRENT APPLICATION NUMBER: US/10/364,276
; PRIOR FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: 09/092,671
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 08/280,864
; PRIOR FILING DATE: 1994-07-26
; PRIOR APPLICATION NUMBER: 09/640,090
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-364-276-12

Query Match      100.0%; Score 117; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23
Db 1 QRVLEIGRTECVLSNLGRTRY 23

RESULT 4
US-10-287-971-48
```

```
; Sequence 48, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: Curaseq1ist version 0.1
; SEQ ID NO 48
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-971-48

Query Match      100.0%; Score 117; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEIGRTECVLSNLGRTRY 23
Db 194 QRVLEIGRTECVLSNLGRTRY 216

RESULT 5
US-10-287-971-50
; Sequence 50, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: Curaseq1ist version 0.1
; SEQ ID NO 50
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-287-971-50
Query Match      100.0%; Score 117; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGRTRY 23
Db 194 QRVLEGRTECVLSNLRGRTRY 216

RESULT 6
US-10-287-971-52
Sequence 52, Application US/10287971
Publication No. US20040067882A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, et al
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-480A
CURRENT APPLICATION NUMBER: US/10/287,971
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 09/997,425
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 10/035,568
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/338,626
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 60/401,479
PRIOR FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: 60/333,072
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/348,283
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 60/393,262
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/406,181
PRIOR FILING DATE: 2002-08-26
SOFTWARE: Curasequest version 0.1
SEQ ID NO 52
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-971-52

Query Match      100.0%; Score 117; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGRTRY 23
Db 194 QRVLEGRTECVLSNLRGRTRY 216

RESULT 7
US-09-016-159-5
Sequence 5, Application US/09016159
Patent No. US20020031806A1
GENERAL INFORMATION:
APPLICANT: Lee, Jong Y.
TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq For Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,159
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/876,227
FILING DATE: 16-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/734,097
FILING DATE: 21-OCT-1996
APPLICATION NUMBER: 08/460,525
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07004/002003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/335-5070
TELEFAX: 612/288-9696
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 508 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-159-5

Query Match      100.0%; Score 117; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRVLEGRTECVLSNLRGRTRY 23
Db 194 QRVLEGRTECVLSNLRGRTRY 216

RESULT 8
US-10-287-971-54
Sequence 54, Application US/10287971
Publication No. US20040067882A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, et al
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METIC
FILE REFERENCE: 21402-480A
CURRENT APPLICATION NUMBER: US/10/287,971
CURRENT FILING DATE: 2002-11-05
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 10/035,568
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/338,626
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 60/401,479
PRIOR FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: 60/333,072
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/348,283
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 60/393,262
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/406,181
PRIOR FILING DATE: 2002-08-26
SOFTWARE: Curasequest version 0.1
SEQ ID NO 54
LENGTH: 508
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-971-54

Query Match      96.6%; Score 113; DB 12; Length 508;
```

Best Local Similarity 95.7%; Pred. NO. 2.7e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRVLEGRTECVLSNLRGRTRY 23
DB 194 QRVLEGRTECVLSNLRGRTRY 216

RESULT 9
US-10-316-194-142
; Sequence 142, Application US/10316194
; Publication No. US20030215914A1
; GENERAL INFORMATION:
; APPLICANT: Houtzager, Erwin
; APPLICANT: Vijjn, Irma M.C.
; APPLICANT: Sijmons, Peter C.
; TITLE OF INVENTION: A structure for presenting desired peptide sequences
; FILE REFERENCE: 2183-5610US
; CURRENT APPLICATION NUMBER: US/10/316,194
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/016,516
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 142
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IMABIS020
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(109)
US-10-316-194-142

Query Match 88.0%; Score 103; DB 15; Length 109;
Best Local Similarity 91.3%; Pred. No. 1.8e-08;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 QRVLEGRTECVLSNLRGRTRY 23
DB 46 QRVLEGRTECVLSNLRGRTRY 68

RESULT 10
US-10-316-194-144
; Sequence 144, Application US/10316194
; Publication No. US20030215914A1
; GENERAL INFORMATION:
; APPLICANT: Houtzager, Erwin
; APPLICANT: Vijjn, Irma M.C.
; APPLICANT: Sijmons, Peter C.
; TITLE OF INVENTION: A structure for presenting desired peptide sequences
; FILE REFERENCE: 2183-5610US
; CURRENT APPLICATION NUMBER: US/10/316,194
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/016,516
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 144
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IMABIS027
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(109)
US-10-316-194-144

Query Match 82.1%; Score 96; DB 15; Length 109;
Best Local Similarity 87.0%; Pred. No. 2.3e-07;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QRVLEGRTECVLSNLRGRTRY 23
DB 46 QRVLEGRTECVLSNLRGRTRY 68

RESULT 11
US-10-316-194-35
; Sequence 35, Application US/10316194
; Publication No. US20030215914A1
; GENERAL INFORMATION:
; APPLICANT: Houtzager, Erwin
; APPLICANT: Vijjn, Irma M.C.
; APPLICANT: Sijmons, Peter C.
; TITLE OF INVENTION: A structure for presenting desired peptide sequences
; FILE REFERENCE: 2183-5610US
; CURRENT APPLICATION NUMBER: US/10/316,194
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/016,516
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 35
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid
; OTHER INFORMATION: sequence of iMab600
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(109)
US-10-316-194-35

Query Match 79.5%; Score 93; DB 15; Length 109;
Best Local Similarity 87.0%; Pred. No. 6.7e-07;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QRVLEGRTECVLSNLRGRTRY 23
DB 46 QRVLEGRTECVLSNLRGRTRY 68

RESULT 12
US-10-316-194-43
; Sequence 43, Application US/10316194
; Publication No. US20030215914A1
; GENERAL INFORMATION:
; APPLICANT: Houtzager, Erwin
; APPLICANT: Vijjn, Irma M.C.
; APPLICANT: Sijmons, Peter C.
; TITLE OF INVENTION: A structure for presenting desired peptide sequences
; FILE REFERENCE: 2183-5610US
; CURRENT APPLICATION NUMBER: US/10/316,194
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/016,516
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 43
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid
; OTHER INFORMATION: sequence of iMab1100
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(109)
US-10-316-194-43

Query Match 73.5%; Score 86; DB 15; Length 109;

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